

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 08:33:07 ; Search time 1398.42 Seconds

(without alignments)
11033.514 Million cell updates/sec

Title: US-09-727-855B-1

Perfect score: 3632

Sequence: 1 tctgttgataatcttctta.....aagagcttgacattgtag 3632

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001s:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84.2	2.3	728	2 AAT85876	Aat85876 Malassezia
2	78.8	2.2	897	9 ADD35245	Add35245 Mouse mlt
3	74	2.0	270	7 AAT33645	Abt33645 Anticance
4	74	2.0	627	2 AAT70431	Aag70431 MHS:MnSOD
5	74	2.0	666	6 AAT09580	Abt09580 Phase-1 R
6	74	2.0	813	2 AAT053193	Aag053193 MnSOD cdn
7	74	2.0	813	2 AAT15589	Aat15589 Human man
8	74	2.0	813	2 AAT34277	Aat34277 Human man
9	74	2.0	813	2 AAT24998	Aax24998 Human nat
10	74	2.0	813	3 AAT63891	Aag63891 CDNA enco
11	74	2.0	849	6 AAT84891	Abn84891 Human man
12	74	2.0	849	6 AAT94453	Aaa94453 Human man
13	74	2.0	930	9 AAT76309	Ade76309 Human BSK
14	74	2.0	972	7 AAT63836	Abx63836 Human cdn
15	74	2.0	1026	6 AAT66512	Abt66512 Lung canc
16	74	2.0	1026	6 AAT84524	Abk84524 Human cdn
17	74	2.0	1046	2 AAT94284	Aag94284 Human man
18	74	2.0	1438	3 AAT75734	Aaa75734 Nucleotid
19	74	2.0	1492	6 AAT63720	Abk63720 Rat seque
20	74	2.0	1492	9 AAT58236	Adb58236 Toxicity-
21	74	2.0	2504	4 AAT26545	Aal26545 Human bre
22	73	2.0	325	6 AAT39690	Aad39690 Human Mns
23	73	2.0	414	3 AAT02178	Aac02178 Human sec

24	72.6	2.0	424	7 ABX49579	Abx49579 Bovine ES
25	72.4	2.0	594	3 AAT39779	Aaz39779 Human man
26	72.4	2.0	609	2 AAT20194	Aaq20194 Mn-SOD (I
27	72.4	2.0	627	2 AAT70432	Aag70432 MHS:MnSO
28	72.4	2.0	681	3 AAT39781	Aaz39781 Human man
29	72.4	2.0	813	1 AAT71370	Aan71370 Sequence
30	72.4	2.0	813	1 AAT81158	Aan81158 cDNA enco
31	72.4	2.0	969	2 AAT31018	Aat31018 Human man
32	72.4	2.0	976	2 AAT67474	Aaq67474 Human man
33	72.4	2.0	976	2 AAT33940	Aax33940 Human HCM
34	72.4	2.0	976	2 AAT08429	Aax08429 Human man
35	72.4	2.0	976	7 AAT83721	Abz83721 Toxicolog
36	72.4	2.0	3789	3 AAT39782	Aaz39782 Plasmid p
37	71	2.0	2208	7 ABX63709	Abx63709 Human cdn
38	71	2.0	3300	2 AAT31822	Aav31822 Mutant As
39	71	2.0	3300	2 AAT20707	Aaz20707 A. oryzae
40	71	2.0	3300	6 AAT93439	Aba93439 Mutant As
41	70.8	1.9	977	2 AAT73824	Aav73824 Human SOD
42	70.6	1.9	631	7 ABZ56304	Abz56304 Aspergill
43	70.6	1.9	702	3 AAT14076	Aaf14076 Aspergill
44	68.6	1.9	2809	9 ADB68898	Adb68898 C. neofo
45	68.2	1.9	894	9 ADE25718	Ade25718 Human cdn

ALIGNMENTS

RESULT 1
AAT85876

ID AAT85876 standard; cDNA to mRNA; 728 BP.

XX AC AAT85876;

XX DT 27-AUG-2003 (revised)

DT 23-FEB-1998 (first entry)

XX DE Malassezia fungus MF-3 antigenic protein encoding cDNA.

XX KW Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;

XX KW allergy; antigen; ds.

XX OS Malassezia.

XX FH Key Location/Qualifiers

FT CDS 4..621

FT /*tag= a

FT /product= "MR-3_antigenic_protein"

XX WO9721817-A1.

XX PD 19-JUN-1997.

XX PF 10-DEC-1996; 96WO-JP003602.

XX PR 12-DEC-1995; 95JP-00346627.

XX PR 05-SEP-1996; 96JP-00257612.

XX PR 05-SEP-1996; 96JP-00257613.

XX (TAKI) TAKARA SHUZO CO LTD.

XX Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;

XX Akiyama K, Yaeueda H, Yamaguchi H;

XX WPI; 1997-332788/30.

XX P-PSDB; AAW29770.

XX Antigenic proteins from the fungus Malassezia - bind to IgG antibodies

XX Present in patients with Malassezia allergies, useful for diagnosis,

XX treatment and prevention of such conditions.

XX Claim 53; Page 76-77; 162pp; Japanese.

XX The present sequence encodes a specifically claimed antigenic protein

XX WPI; 2003-210360/20.
 XX
 PT DNA array for measuring expression of a number of different target gene
 PT fragments for measuring sensitivity of tumors to anticancer agents.
 XX
 PS Disclosure; Page 73; 83pp; Japanese.
 XX
 CC The invention relates to a novel DNA array for measuring sensitivity of a
 CC tumour to an anticancer agent comprising at least thirteen different
 CC target gene fragments selected from at least two types of gene including
 CC genes for, enzymes associated with nucleic acid metabolism, gene repair,
 CC factors associated with drug tolerance, and housekeeping genes. The array
 CC is used for large-scale gene-expression profiling, especially for
 CC assaying the sensitivity of tumours to anti-cancer agents. This
 CC polynucleotide sequence represents a target gene fragment of the
 CC invention
 XX
 SQ Sequence 270 BP; 72 A; 86 C; 66 G; 46 T; 0 U; 0 Other;
 Query Match 2.0%; Score 74; DB 7; Length 270;
 Best Local Similarity 67.5%; Pred. No. 3.2e-11;
 Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACACACCAAGCACCATCAG 1366
 Db 54 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACACACCAAGCACCATCAG 113
 QY 1367 ACTTATGTTAAACGGCTCAACGCTGCGGAGGAGCTACTCGGCGGTGTGGCAAGGAG 1426
 Db 114 GCCTAGTGAACACCTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 173
 QY 1427 GATGTGCTTACCAGGTTAAAGCTTCAAGTCTGAGTCTGTAC 1460
 Db 174 GATGTTACAGCCAGATAGCTCTTCAGCTGCAC 207
 RESULT 4
 AAQ70431
 ID AAQ70431 standard; DNA; 627 BP.
 AC AAQ70431;
 XX
 XX 25-MAR-2003 (revised)
 DT 28-FEB-1995 (first entry)
 XX
 DE MHS:MnSOD variant.
 XX
 KW Manganese superoxide dismutase; MnSOD; oxygen; cosmetic; mutation;
 KW arthritis; variant; enzyme; isoelectric point; inflammation; cancer;
 KW premature retinopathy; hypertension; diabetes; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..606
 FT /*tag= a
 FT misc_difference 406..408
 FT /*tag= b
 FT /transl_except= pos:406..408, aa:Gly
 XX
 PN WO9414950-A1.
 XX
 XX 07-JUL-1994.
 XX
 XX 28-DEC-1993; 93WO-JP001917.
 XX
 XX 28-DEC-1992; 92JP-00359959.
 XX
 XX (SIIT-) SII TECHNORESEARCH INC.
 XX
 XX Kondo M, Katsuta K;
 XX

DR WPI; 1994-234688/28.
 DR P-PSDB; AAR60360.
 XX
 PT Human variant manganese super-oxide dismutase with aminoacid mutation in
 PT non-essential regions - for treatment of arthritis, active oxygen related
 PT disorders and for cosmetics.
 XX
 PS Example 3; Page 16-17; 34pp; Japanese.
 XX
 CC Human variant manganese superoxide dismutase (Mn-SOD) comprises an amino
 CC acid substitution in a region which does not affect enzyme activity, of a
 CC positively charged amino acid residue, which has the effect of raising
 CC the isoelectric point of the peptide. These Mn-SOD variants are useful as
 CC medical preps. for the treatment of human arthritis and diseases caused
 CC by active oxygen, and as cosmetic preps. They are also useful for
 CC treatment of inflammation, cancer, premature retinopathy, hypertension
 CC and diabetes. Examples of variant Mn-SODs are given in AAQ70431-32.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 627 BP; 175 A; 152 C; 160 G; 140 T; 0 U; 0 Other;
 Query Match 2.0%; Score 74; DB 2; Length 627;
 Best Local Similarity 67.5%; Pred. No. 5.6e-11;
 Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACACCAAGCACCATCAG 1366
 Db 46 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCCACACCAAGCACCATCAG 105
 QY 1367 ACTTATGTTAAACGGCTCAACGCTGCGGAGGAGCTACTCGGCGGTGTGGCAAGGAG 1426
 Db 106 GCCTAGTGAACACCTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 165
 QY 1427 GATGTGCTTACCAGGTTAAAGCTTCAAGTCTGAGTCTGTAC 1460
 Db 166 GATGTTACAGCCAGATAGCTCTTCAGCTGCAC 199
 RESULT 5
 ABT09580
 ID ABT09580 standard; DNA; 666 BP.
 XX
 AC ABT09580;
 XX
 DT 05-DEC-2002 (first entry)
 XX
 DE Phase-1 Rat CT gene SEQ ID No 668.
 XX
 KW Rat; toxicity study; rat toxic response gene; toxicological response;
 KW drug development; phase-1 rat CT gene; ds.
 XX
 OS Rattus sp.
 XX
 PN WO200266682-A2.
 XX
 PD 29-AUG-2002.
 XX
 PF 29-JAN-2002; 2002WO-US002935.
 XX
 PR 29-JAN-2001; 2001US-0264933P.
 PR 26-JUL-2001; 2001US-0308161P.
 XX
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 XX
 PI Farris G, Hicklen SH, Farr SB;
 XX
 XX WPI; 2002-674961/72.
 XX
 PT Evaluating the toxicity of an agent, useful in drug development or in
 PT determining toxicological responses to a new drug, by determining the
 PT expression of rat toxicologically relevant genes in the test animal in
 PT response to the test agent.
 XX

PS Disclosure; Page 270; 388pp; English.

XX The invention relates to a method used for evaluating the toxicity of an

CC agent comprising determining the expression of a rat toxic response

CC gene(s) in the test animal in response to the agent. The method is useful

CC in drug development, particularly for conducting toxicity studies and

CC analysis before a new drug or compound is approved for human consumption

CC or use. The method is also useful in determining toxicological responses

CC to a new drug. This polynucleotide sequence represents a phase-1 rat CT

CC gene of the invention

XX

SQ Sequence 666 BP; 172 A; 164 C; 182 G; 146 T; 0 U; 2 Other;

Query Match 2.0%; Score 74; DB 6; Length 666;

Best Local Similarity 67.5%; Pred. No. 5.9e-11;

Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

OY 1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCCTTCCACCAAGCACCACATCAG 1366

DB 124 GCGCTGGAGCCGACATTTACGGCGAGATCATGCGAGCTGCACCAAGCACCACGCG 183

OY 1367 ACTTATGTATACGGCTCAAGCTGCCGAGGAGAGCTACTGCGCGCTGTGGGCAAGGAG 1426

DB 184 ACCTACGTGAACAATCTGACGTCACCGAGGAGAGTACCAAGGCGCTGGCCAAAGGGA 243

OY 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460

DB 244 GATGTTACAATCAGGTGCTTCTTACGCTGCAC 277

RESULT 6

AAQ53193

ID AAQ53193 standard; cDNA; 813 BP.

XX

AC AAQ53193;

DT 25-MAR-2003 (revised)

DT 21-JUN-1994 (first entry)

XX

DE MnSOD cDNA.

XX

MnSOD; manganese superoxide dismutase; N-terminal; catalyst; reperfusion;

KW injury; ischaemia; superoxide; SO; molecular oxygen; anti-inflammatory;

KW ss.

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

PH 43..711

FT /*tag= a

FT /product= "MnSOD"

FT

XX US5270195-A.

XX

PD 14-DEC-1993.

XX

PF 10-JUL-1992; 92US-00912213.

XX

PR 22-NOV-1985; 85US-00801090.

PR 12-SEP-1986; 86US-00907051.

PR 29-OCT-1986; 86IE-00002851.

PR 27-MAR-1987; 87US-00032734.

PR 13-DEC-1989; 89US-00453057.

XX

(BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX

Beck Y, Hartman JR;

XX

PI 1993-404931/50.

DR P-PSDB; AAR44801.

XX

Expression plasmid in Escherichia coli host system - encodes human

XX manganese superoxidizedismutase analogue, useful for e.g. treating

PT

inflammation.

XX

Claim 1; Fig 1a-1c; 27pp; English.

XX

The sequence encodes a manganese superoxide dismutase which can be used to

CC catalyse the reduction of superoxide (SO) radicals to hydrogen peroxide

CC and molecular oxygen. It can be used to reduce reperfusion injury

CC following ischaemia and prolong the survival of excised organs. It can

CC also be used as a long acting anti-inflammatory drug. (Updated on 25-MAR-

CC 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)

XX

SQ Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;

Query Match 2.0%; Score 74; DB 2; Length 813;

Best Local Similarity 67.5%; Pred. No. 6.7e-11;

Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

OY 1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCCTTCCACCAAGCACCACATCAG 1366

DB 151 GCCCTGGAACTCATCAACGCGAGATCATGCGAGCTGCACCAAGCACCACGCG 210

OY 1367 ACTTATGTATACGGCTCAAGCTGCCGAGGAGAGCTACTGCGCGCTGTGGGCAAGGAG 1426

DB 211 GCCTACGTGAACAATCTGACGTCACCGAGGAGAGTACCAAGGCGCTGGCCAAAGGGA 270

OY 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460

DB 271 GATGTTACAGCCGAGATAGCTTTCAGCTGCAC 304

RESULT 7

AAT15589

ID AAT15589 standard; cDNA; 813 BP.

XX

AC AAT15589;

DT 25-MAR-2003 (revised)

DT 06-APR-1996 (first entry)

XX

DE Human manganese superoxide-dismutase cDNA.

XX

Human; manganese superoxide-dismutase; T-lymphocyte; probe; cDNA;

KW Escherichia coli; plasmid pMS8-4; N-terminal truncation; cloning;

KW aminopeptidase; antiinflammatory; oxygen free radical scavenger;

KW synovial inflammation; arthritis; lung fibrosis; ds.

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

PH 43..711

FT /*tag= a

FT /product= "Manganese superoxide-dismutase"

FT /note= "EC-1.15.1.1"

FT sig_peptide 43..114

FT /*tag= b

FT mat_peptide 115..708

FT /*tag= c

XX

EP691401-A1.

XX

PD 10-JAN-1996.

XX

PF 25-MAR-1988; 95EP-00106995.

XX

PR 27-MAR-1987; 87US-00032734.

PR 26-FEB-1988; 88US-00161117.

XX

(BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX

Hartman JR, Beck Y, Nimrod A;

XX

PI 1996-059735/07.

DR P-PSDB; AAR90713.

XX New human manganese superoxide dismutase analogues - having a Lys and
PT opt. His residue absent from the N-terminus, useful for treating e.g.
PT synovial inflammation, arthritis or lung fibrosis.
XX Example 1; Fig 1; 45pp; English.
XX The sequence encodes a human manganese superoxide-dismutase (MnSOD), and
CC has been isolated from a human T-lymphocyte cDNA library in phage lambda-
CC gt10 in Escherichia coli, by screening with a 5'-probe (AAT15591) and a
CC 3'-probe (AAT15592). The sequence of the insert in plasmid pMS8-4
CC (obtained by subcloning in plasmid pBR322) is shown. The cDNA may be
CC expressed in e.g. E. coli for production of recombinant MnSOD. The MnSOD
CC product may be cleaved with Aeromonas proteolytica aminopeptidase to
CC produce an N-terminally truncated analogue with lysine and optionally
CC histidine residues removed. The MnSOD analogue may be used in therapy of
CC conditions associated with generation of oxygen free radicals,
CC particularly synovial inflammation, arthritis and lung fibrosis.
CC (claimed). (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 74; DB 2; Length 813;
Best Local Similarity 67.5%; Pred. No. 6.7e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCAACACCAAGCACCACATCAG 1366
Db 151 GCCTGGAGACCTCACATCAACGCGAGATCATGCTGCACACAGCAGCACCACGCG 210
QY 1367 ACTTATGTTAAGCGCTCAACGCTGCCGAGGAGTACTTCGCGCGCTGTGGCAAGGAG 1426
Db 211 GCCTAGCTGAACAACCTGAACGTCACCGAGGAGAGTACCAGGAGGCTTGGCCAGGGA 270
QY 1427 GATGTCCTTACCAGGTTAAGCTTCACTCTGTCTGTAC 1460
Db 271 GATGTTACAGCCAGATAGCTCTTTCAGCTGCAC 304
RESULT 8
AAT34277
ID AAT34277 standard; cDNA; 813 BP.
AC AAT34277;
XX
XX 25-MAR-2003 (revised)
DT 24-OCT-1996 (first entry)
XX
XX Human manganese superoxide dismutase cDNA.
DE Manganese superoxide dismutase; MnSOD; reperfusion injury; ischaemia;
KW bronchial pulmonary dysplasia; inflammation; antiinflammatory; ds.
XX
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 43..711
FT /*tag= a
FT sig_peptide 43..114
FT /*tag= b
FT mat_peptide 115..708
FT /*tag= c
XX
XX US5540911-A.
XX
XX 30-JUL-1996.
XX
XX 09-JAN-1995; 95US-00370461.
XX
XX 22-NOV-1985; 85US-00801090.
PR 12-SEP-1986; 86US-00907051.
PR 29-OCT-1986; 86IE-00002851.
PR 27-MAR-1987; 87US-00032734.

PR 13-DEC-1989; 89US-00453057.
PR 10-JUL-1992; 92US-00912213.
BR 14-SEP-1993; 93US-00120551.
XX
PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX
XX Hartman JR, Beck Y;
PI
XX WPI; 1996-361912/36.
DR P-PSDB; AAW00018.
XX
XX Use of recombinant human manganese superoxide dismutase - for treating
PT inflammation or bronchial pulmonary dysplasia, reducing reperfusion
PT injury or prolonging organ survival.
XX
XX Claim 1; Fig 1A-1C; 27pp; English.
XX A cDNA clone (AAT34277) codes for human manganese superoxide dismutase
CC (MnSOD) (AAW00018), an enzyme that catalyses the reduction of superoxide
CC radicals to H2O2 and O2. It was isolated from a human T-cell library
CC cloned into vector gt10 using probes (see also AAT34283-84) based on
CC portions of mature MnSOD. The MnSOD gene was also identified (see also
CC AAT34278-82). The cDNA can be used for the prodn. of recombinant MnSOD
CC using e.g. Escherichia coli cells as hosts. The MnSOD is useful for
CC reducing reperfusion injury, treating inflammation or bronchial pulmonary
CC dysplasia and for prolonging survival of excised organs. (Updated on 25-
CC MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
CC field.)
XX
XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 74; DB 2; Length 813;
Best Local Similarity 67.5%; Pred. No. 6.7e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCCCTTCAACACCAAGCACCACATCAG 1366
Db 151 GCCTGGAGACCTCACATCAACGCGAGATCATGCTGCACACAGCAGCACCACGCG 210
QY 1367 ACTTATGTTAAGCGCTCAACGCTGCCGAGGAGTACTTCGCGCGCTGTGGCAAGGAG 1426
Db 211 GCCTAGCTGAACAACCTGAACGTCACCGAGGAGAGTACCAGGAGGCTTGGCCAGGGA 270
QY 1427 GATGTCCTTACCAGGTTAAGCTTCACTCTGTCTGTAC 1460
Db 271 GATGTTACAGCCAGATAGCTCTTTCAGCTGCAC 304
RESULT 9
AAX24998
ID AAX24998 standard; cDNA; 813 BP.
XX
XX AAX24998;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human native manganese superoxide dismutase cDNA.
DE Superoxide dismutase; MnSOD; SOD; human; protein engineering;
KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
KW inflammation; reperfusion injury; therapy; ss.
XX
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 43..711
FT /*tag= a
FT sig_peptide 43..114
FT /*tag= b
FT mat_peptide 115..708
FT /*tag= c
XX
XX WO913088-A1.

XX 18-MAR-1999.
 PD 10-SEP-1998; 98WO-US018842.
 XX 10-SEP-1997; 97US-00927230.
 XX (UYFL) UNIV FLORIDA.
 PA Nick HS, Silverman DN;
 FI WPI; 1999-229242/19.
 DR P-PSDE; AAW98169.
 XX New recombinant human manganese superoxide dismutase proteins.
 PT Disclosure; Page 52-53; 61pp; English.
 XX This cDNA sequence codes for human manganese superoxide dismutase
 CC (hMnSOD, see AAW98169). Novel MnSOD proteins having catalytic activity
 CC which differs from this natural hMnSOD are claimed. The modified proteins
 CC exhibit reduced or no product inhibition, or have greater activity, or
 CC both, compared to natural hMnSOD. The modifications involve one or amino
 CC acid substitutions within the active site of the enzyme, especially at
 CC residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and
 CC His-163 (see also AAW98171-77). Nucleic acids encoding the modified
 CC hMnSOD proteins are also claimed. The modified hMnSOD proteins, or
 CC expression vectors in which modified hMnSOD nucleic acid is linked to a
 CC promoter (preferably mammalian), can be used to protect a cell line from
 CC damage caused by superoxide radicals (claimed). They can also be used to
 CC treat subjects suffering from, or at risk of, cytotoxicity caused by
 CC superoxide radicals (claimed). As such, they can be used as antioxidants
 CC in the treatment of a variety of disorders, including inflammation
 CC (claimed), reperfusion injury following ischemia (claimed), and cellular
 CC damage caused by chemotherapeutic agents
 XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
 SQ
 Query Match 2.0%; Score 74; DB 2; Length 813;
 Best Local Similarity 67.5%; Pred. No. 6.7e-11;
 Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCTTCCACCACCAAGCACCATCAG 1366
 Db 151 GCCCTGGAACCTCATCAACGCGCAGATCATGCGCTGCACCAAGCACCACGCG 210
 QY 1367 ACTTATGTTAAGGCTCAAGCTCCGAGGAGAGCTACTGCGCGCTGTGGGCAAGAG 1426
 Db 211 GCCTACGTGAACACCTGAACGTCAACGAGGAGAGTACAGGCGCTTGGCCAAAGGA 270
 QY 1427 GATGTGCTTACCAGGTTAAGCTTCAGTCTGTAC 1460
 Db 271 GATGTACGCCAGATAGCTCTTCAGCTGTGCAC 304
 RESULT 10
 ID AAW63891
 XX AAAC63891 standard; cDNA; 813 BP.
 XX AAAC63891;
 AC
 DT 04-DEC-2000 (first entry)
 XX cDNA encoding a human manganese superoxide dismutase.
 DE Human; manganese superoxide dismutase; hMn SOD; superoxide radical;
 XX superoxide radical damage; cytotoxicity; inflammation; ischemia;
 KW reperfusion injury; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 43..711
 FT CDS

FT /*tag= a
 FT /transl_except= (pos: 505..507, aa: Xaa)
 FT /transl_except= (pos: 511..513, aa: Ala)
 FT /product= "manganese superoxide dismutase"
 FT /note= "Xaa is Gln or Glu"
 FT 43..114
 FT /*tag= b
 FT 115..708
 FT /*tag= c
 FT sig_peptide
 FT mat_peptide
 XX US6107070-A.
 PN 22-AUG-2000.
 XX 10-SEP-1998; 98US-00151052.
 PF 10-SEP-1997; 97US-00927230.
 PR (UYFL) UNIV FLORIDA.
 PA Silverman DN, Nick HS;
 PI WPI; 2000-578537/54.
 DR P-PSDB; AAB08204.
 XX Novel human manganese superoxide dismutase protein useful as antioxidant
 PT for treating cytotoxicity caused by superoxide radicals, inflammation and
 PT reperfusion injury following ischemia.
 XX Disclosure; Col 25-26; 27pp; English.
 PS The present sequence encodes a human manganese superoxide dismutase
 CC protein (hMn SOD). The specification describes a modified hMn SOD which
 CC has a catalytic activity which differs from natural hMn SOD in that it
 CC exhibits reduced or no product inhibition compared to natural hMn SOD.
 CC The natural hMn SOD is especially modified with one or more substitutions
 CC in amino acids 26, 30, 34, 74, 143, 159, 161 and 163. The modified hMn
 CC SOD is useful for protecting a cell from damage caused by superoxide
 CC radicals and for treating a subject suffering from cytotoxicity caused by
 CC superoxide radicals. The protein is useful for treating inflammation and
 CC reperfusion injury following ischemia
 XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
 SQ
 Query Match 2.0%; Score 74; DB 3; Length 813;
 Best Local Similarity 67.5%; Pred. No. 6.7e-11;
 Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 1307 GCCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCTTCCACCACCAAGCACCATCAG 1366
 Db 151 GCCCTGGAACCTCATCAACGCGCAGATCATGCGCTGCACCAAGCACCACGCG 210
 QY 1367 ACTTATGTTAAGGCTCAAGCTCCGAGGAGAGCTACTGCGCGCTGTGGGCAAGAG 1426
 Db 211 GCCTACGTGAACACCTGAACGTCAACGAGGAGAGTACAGGCGCTTGGCCAAAGGA 270
 QY 1427 GATGTGCTTACCAGGTTAAGCTTCAGTCTGTAC 1460
 Db 271 GATGTACGCCAGATAGCTCTTCAGCTGTGCAC 304
 RESULT 11
 ID AAW84891
 XX AAW84891 standard; cDNA; 849 BP.
 XX AAW84891;
 AC
 DT 15-NOV-2002 (first entry)
 XX Human manganese superoxide dismutase gene.
 XX Superoxide dismutase; SOD; hSODm; enzyme; human; osteopathic;
 KW antirheumatic; antiarthritic; vasotropic; antiinflammatory; gene; ss.

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XX OS Homo sapiens.
XX FH Key
XX FT misc_feature
XX FT Location/Qualifiers
XX FT 1..8
XX FT /tag= a
XX FT /note= "EcoRI linker used in cloning"
XX FT CDS
XX FT 100..768
XX FT /tag= b
XX FT /product= "hsODm"
XX FT sig_peptide
XX FT 100..171
XX FT /tag= c
XX FT mat_peptide
XX FT 172..765
XX FT /tag= d
XX FT misc_feature
XX FT 842..849
XX FT /tag= e
XX FT /note= "EcoRI linker used in cloning"
XX US2002081287-A1.
XX 27-JUN-2002.
XX 11-JUN-2001; 2001US-00878589.
XX 14-OCT-1986; 86US-00918534.
XX (CHIR ) CHIRON CORP.
XX Hallelwell RA, Bell GI, Mullenbach GT;
XX WPI; 2002-626527/67.
XX P-PSDB; ABB79798.
XX Preparing recombinant human manganese superoxide dismutase, useful in the
XX treatment of osteoarthritis and rheumatoid arthritis.
XX Example 1; Fig 4; 16pp; English.
XX The present sequence is the nucleotide sequence of human manganese
XX superoxide dismutase (hsODm) cDNA. The cDNA was isolated from an adult
XX human kidney cDNA library in lambda-gt10 using the probes given in
XX CC A8N84889-90. The invention relates to methods for hsODm gene cloning and
XX CC expression in microorganisms, especially Escherichia coli or
XX CC Saccharomyces cerevisiae. The hsODm cDNA is inserted into a vector for
XX CC expression in the microbial host, preferably under conditions which allow
XX CC for processing to remove the N-terminal methionine. The expression
XX CC product is useful for treating a patient having inflammatory joint
XX CC disease (e.g. osteoarthritis or rheumatoid arthritis), or to minimise
XX CC post-ischaemic tissue damage resulting from disease or surgery
XX SQ Sequence 849 BP; 256 A; 197 C; 227 G; 169 T; 0 U; 0 Other;
Query Match 2.0%; Score 74; DB 6; Length 849;
Best Local Similarity 67.5%; Pred. No. 6.9e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCTCGAGCGCTCCATCTCCAGGAGATCATGACCTTCACACACCAAGCACCATCAG 1366
DB 208 GCCTCGAGCGCTCCATCTCCAGGAGATCATGACCTTCACACACCAAGCACCAGCG 267
QY 1367 ACTTATGTGTTAAACGGCTCAACGGTCCGAGGAGAGTACTCGGCGCGTGTGGGCAAGGAG 1426
DB 268 GCCTAGCTGACCACTGAACCTGACCGTCCACCGAGGAGAGTACCAAGGCGGTGGCCAGGGA 327
QY 1427 GATGTGCTTACCCAGGTTAAGCTTCAAGTCTGTATC 1460
DB 328 GATGTTACAGCCAGATAGCTCTTCAGCCTGCAC 361

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RESULT 12
ABA94453
ID ABA94453 standard; cDNA; 849 BP.
XX

```

AC ABA94453;
XX 09-APR-2002 (first entry)
XX Human manganese superoxide dismutase (hsODm) encoding cDNA.
XX DE Human manganese superoxide dismutase; antiinflammatory; antiarthritic;
XX KW antirheumatic; vasotropic; osteopathic; hsODm; human; ss.
XX OS Homo sapiens.
XX FH Key
XX FT CDS
XX FT Location/Qualifiers
XX FT 100..768
XX FT /tag= a
XX FT /product= "hsODm"
XX FT sig_peptide
XX FT 100..171
XX FT /tag= b
XX FT mat_peptide
XX FT 172..765
XX FT /tag= c
XX US6326003-B1.
XX 04-DEC-2001.
XX 14-OCT-1986; 86US-00918534.
XX 14-OCT-1986; 86US-00918534.
XX (CHIR ) CHIRON CORP.
XX Hallelwell RA, Bell GI, Mullenbach GT;
XX WPI; 2002-129495/17.
XX P-PSDB; ABB07330.
XX Treating inflammatory joint disease such as osteoarthritis, rheumatoid
XX arthritis and post ischemic tissue injury, comprises injecting human
XX manganese superoxide dismutase.
XX Example 2; Fig 4; 14pp; English.
XX The invention relates to a method of treating a patient with inflammatory
XX joint disease. The method involves intra-articularly injecting into the
XX afflicted joint a solution of human manganese superoxide dismutase
XX (hsODm). The treatment is used to treat an inflammatory joint disease,
XX particularly osteoarthritis or rheumatoid arthritis. The method can also
XX be used to treat post ischemic tissue injury. The present sequence
XX represents a cDNA encoding the hsODm
XX SQ Sequence 849 BP; 256 A; 197 C; 227 G; 169 T; 0 U; 0 Other;
Query Match 2.0%; Score 74; DB 6; Length 849;
Best Local Similarity 67.5%; Pred. No. 6.9e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCTCGAGCGCTCCATCTCCAGGAGATCATGACCTTCACACACCAAGCACCATCAG 1366
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QY 1367 ACTTATGTGTTAAACGGCTCAACGGTCCGAGGAGAGTACTCGGCGCGTGTGGGCAAGGAG 1426
DB 268 GCCTAGCTGACCACTGAACCTGACCGTCCACCGAGGAGAGTACCAAGGCGGTGGCCAGGGA 327
QY 1427 GATGTGCTTACCCAGGTTAAGCTTCAAGTCTGTATC 1460
DB 328 GATGTTACAGCCAGATAGCTCTTCAGCCTGCAC 361

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RESULT 13
ADE76309
ID ADE76309 standard; DNA; 930 BP.
XX
AC ADE76309;

XX 29-JAN-2004 (first entry)
XX Human BSK-1H13 complementary strand DNA.
DE monocyte; macrophage; gene expression profile; rheumatoid arthritis;
XX chronic inflammatory disease; bacteria-induced inflammation;
KW arteriosclerosis; tumour; organ; tissue transplant; sepsis;
KW molecular classification; human; BSK; ss.
XX Homo sapiens.
OS EPI1310567-A2.
XX PN 14-MAY-2003.
XX PD 02-OCT-2002; 2002EP-00090348.
XX PF 09-NOV-2001; 2001DE-01055600.
XX PR (OLIG-) OLIGENE GMBH.
XX PA Stuhlmueller B, Haeupl T;
XX PI WPI; 2003-443090/42.
XX DR Device for diagnosis, prognosis and monitoring therapy of e.g. rheumatoid
XX PT arthritis, comprises immobilized gene sequences from monocyte-macrophage
XX PT cells.
XX PS Claim 29; SEQ ID NO 121; 180pp; German.
XX PS The invention relates to a novel device for diagnosis, prognosis and
XX CC monitoring of therapy having, on its surface, sequences of some or all of
XX CC specified monocyte-macrophage genes and also of other genes or RNA
XX CC complementary to the specified genes. The device of the invention may be
XX CC used to determine gene expression profiles for measurement of monocyte or
XX CC macrophage activation or inflammation in blood or other tissues, as well
XX CC as for the diagnosis, prognosis and monitoring therapy in cases of
XX CC rheumatoid arthritis, chronic inflammatory disease, chronic bacteria-
XX CC induced inflammation, arteriosclerosis, tumours, organ or tissue
XX CC transplants and sepsis. The device provides information for molecular
XX CC classification and staging of disease, creation of a patient-specific
XX CC prognostic profile and suggestions about molecular pathogenesis or
XX CC therapeutic effects, thus facilitating the development of new therapeutic
XX CC strategies and pharmacological concepts. The current sequence is that of
XX CC the human BSK DNA of the invention.
XX SQ Sequence 930 BP; 242 A; 208 C; 206 G; 245 T; 0 U; 29 Other;
Query Match 2.0%; Score 74; DB 9; Length 930;
Best Local Similarity 67.5%; Pred. No. 7.4e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCTGGAGCCCTCCATCTCCAAAGAGATCATGACCTTCACCAACCAAGCACCATCAG 1366
Db 67 GCCTGGAGCCCTCCATCTCCAAAGAGATCATGACCTTCACCAACCAAGCACCATCAG 126
QY 1367 ACTTATGTTAAGGCTCAAGCTCCGAGGAGACTACTCGGCGCTGTGGCGAAGGAG 1426
Db 127 GCCTAGTGAAACAACCTGAACCTGACCCGAGGAGAGTAGTACGAGGCGGTGGCCCAAGGA 186
QY 1427 GATGTGCTTACCCAGGTAAAGCTTCAGTCTGTAC 1460
Db 187 GATGTACAGCCAGATAGTCTTTCAGCTGCAC 220
RESULT 14
ID ABX63836
XX ABX63836 standard; cDNA; 972 BP.
AC ABX63836;
XX

DT 26-FEB-2003 (first entry)
XX Human cDNA #836 differentially expressed in activated vascular tissue.
DE Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;
KW hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective;
KW gene therapy; vascular disease; cancer; coronary; artery disease;
KW hypertension; diabetes; pre-eclampsia; restenosis;
KW ischaemia-reperfusion injury; stroke.
XX Homo sapiens.
OS US2002137081-A1.
XX PN 26-SEP-2002.
XX PD 08-JAN-2002; 2002US-00044090.
XX PF 28-JUL-2000; 2000US-0222469P.
XX PR 08-JAN-2001; 2001US-0260483P.
XX PA (BAND/) BANDMAN O.
XX PI Bandman O;
XX PI WPI; 2003-110597/10.
XX DR Combination for diagnosing, staging, treating, or monitoring the
XX PT progression of treatment of a vascular disease, e.g. atherosclerosis,
XX PT comprises several cDNAs that are differentially expressed in activated
XX PT vascular tissue.
XX PS Claim 1; Page; 18pp; English.
XX CC This invention relates to a combination comprising several cDNAs that are
XX CC differentially expressed in activated vascular tissue. The invention also
XX CC discloses a high throughput method for detecting differentially expressed
XX CC cDNAs in a sample. The cDNAs of the invention may have
XX CC antiarteriosclerotic; cytostatic; cardiant; hypotensive; antidiabetic;
XX CC gynaecological; vasotropic and cerebroprotective activities and may be
XX CC used in gene therapy. The cDNAs of the invention may be used in a high-
XX CC throughput methods for detecting differential expression of one or more
XX CC cDNAs in a sample, or screening several molecules or compounds to
XX CC identify a molecule or compound that specifically binds a cDNA of the
XX CC invention. A protein encoded by the cDNA may be used to screen several
XX CC molecules or compounds to identify a ligand that specifically binds to
XX CC the protein, or to produce or purify an antibody to the protein that can
XX CC be used to detect a protein in a sample or purify a natural or
XX CC recombinant protein from a sample. The nucleotides may be useful for
XX CC diagnosing, staging, treating, or monitoring the progression of treatment
XX CC of a vascular disease, e.g. atherosclerosis, cancer, coronary artery
XX CC disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion
XX CC injury, restenosis, or stroke. The cDNAs can also be used for large-scale
XX CC genetic or gene expression analysis of several new nucleic acid
XX CC molecules. Antibodies to the proteins encoded by the cDNAs are useful for
XX CC diagnosing pre-pathologic disorders, and chronic or acute diseases
XX CC associated with abnormalities in the expression, amount or distribution
XX CC of the protein. The present sequence represents a cDNA of the invention
XX CC that is differentially expressed in activated vascular tissue. Note: The
XX CC sequence data for this patent did not form part of the specification, but
XX CC was obtained in electronic format directly from USPTO at
XX CC http://seqdata.uspto.gov/sequence.html?DocID=20020137081
XX SQ Sequence 972 BP; 265 A; 228 C; 252 G; 227 T; 0 U; 0 Other;
Query Match 2.0%; Score 74; DB 7; Length 972;
Best Local Similarity 67.5%; Pred. No. 7.6e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCTGGAGCCCTCCATCTCCAAAGAGATCATGACCTTCACCAACCAAGCACCATCAG 1366
Db 202 GCCTGGAGCCCTCCATCTCCAAAGAGATCATGACCTTCACCAACCAAGCACCATCAG 261

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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	151.4	4.2	669	9 US-09-727-855B-4	Sequence 4, Appli
3	84.2	2.3	728	14 US-10-109-670-3	Sequence 3, Appli
4	74	2.0	972	13 US-10-044-090-836	Sequence 836, App
5	74	2.0	986	14 US-10-198-846-13503	Sequence 13503, A
6	74	2.0	1026	9 US-09-954-456-1822	Sequence 1822, Ap
7	74	2.0	1026	12 US-10-342-887-509	Sequence 509, App
8	74	2.0	1026	12 US-10-342-887-1305	Sequence 1905, Ap
9	74	2.0	1067	10 US-09-971-429B-22	Sequence 22, Appli
10	74	2.0	1492	9 US-09-917-800A-1627	Sequence 1627, Ap
11	74	2.0	2825	14 US-10-198-846-13787	Sequence 13787, A
12	73	2.0	325	9 US-09-993-333-11	Sequence 11, Appli
13	72.6	2.0	424	9 US-09-960-352-14744	Sequence 14744, A
14	71	2.0	2208	13 US-10-044-090-709	Sequence 709, App
15	69.8	1.9	597	9 US-09-727-855B-6	Sequence 6, Appli

C	16	68.6	1.9	2809	15	US-10-320-797-25	Sequence 25, Appli
	17	68.2	1.9	894	14	US-10-247-671-122	Sequence 122, App
	18	67.8	1.9	344	10	US-09-918-995-24298	Sequence 24298, A
	19	66.2	1.8	812	14	US-10-109-670-4	Sequence 4, Appli
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	22	65.2	1.8	3309400	9	US-09-738-626-1	Sequence 1, Appli
	23	63.6	1.8	630	14	US-10-109-670-29	Sequence 29, Appli
	24	60.8	1.7	3375	9	US-09-727-855B-2	Sequence 2, Appli
	25	60.4	1.7	1984	12	US-10-342-887-267	Sequence 267, App
	26	59	1.6	2217	12	US-10-424-599-90403	Sequence 90403, A
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C	45	51	1.4	330	9	US-09-960-352-11115	Sequence 11115, A

ALIGNMENTS

RESULT 1

US-09-727-855B-1
; Sequence 1, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SITOUCHE, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
; TITLE OF INVENTION: MATERIALS THEREOF
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 3632
; TYPE: DNA
; ORGANISM: Phaffia rhodozyma
US-09-727-855B-1

Query Match	100.0%;	Score 3632;	DB 9;	Length 3632;
Best Local Similarity	100.0%;	Pred. No. 0;		
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 QY 3541 ATGAGATGTCAGGATGCTTGTCTTACTGTAGATGGAGAGAGATATCGAAGCAAGAC 3600
 DB |||||
 QY 3541 ATGAGATGTCAGGATGCTTGTCTTACTGTAGATGGAGAGAGATATCGAAGCAAGAC 3600
 DB |||||
 QY 3601 ATACACTTTTGAAGAGCTTGAACCAATTTAG 3632
 DB |||||
 QY 3601 ATACACTTTTGAAGAGCTTGAACCAATTTAG 3632
 DB |||||
 RESULT 2
 US-09-727-855B-4
 ; Sequence 4, Application US/09727855B
 ; Patent No. US20020168703A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HOSHINO, Tatsuo
 ; APPLICANT: OJIMA, Kazuyuki
 ; APPLICANT: SETOGUCHI, Yutaka
 ; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
 ; TITLE OF INVENTION: MATERIALS THEREOF
 ; FILE REFERENCE: C38435/111694
 ; CURRENT APPLICATION NUMBER: US/09/727,855B
 ; CURRENT FILING DATE: 2000-12-01
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 669
 ; TYPE: DNA
 ; ORGANISM: Phaffia rhodozyma
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(666)
 ; OTHER INFORMATION: n or X = A, C, G or T
 US-09-727-855B-4
 Query Match 4.2%; Score 151.4; DB 9; Length 669;
 Best Local Similarity 99.3%; Pred. No. 9.7e-36;
 Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1305 AGGCGCTCGAGCGCTCCATCTCCAGGAGATCATGACCTTCACACACCAAGCACCATC 1364
 DB |||||
 QY 110 ATGCGCTCGAGCGCTCCATCTCCAGGAGATCATGACCTTCACACACCAAGCACCATC 169
 DB |||||
 QY 1365 AGACTTATGTTAAACGCGCTCAACGCTGCGAGAGAGCTTACTCGGCGGCTGTGGCAAG 1424
 DB |||||
 QY 170 AGACTTATGTTAAACGCGCTCAACGCTGCGAGAGAGCTTACTCGGCGGCTGTGGCAAG 229
 DB |||||
 QY 1425 AGGATGCTGTTACCCAGGTTAAGCTTCACTCTG 1457
 DB |||||
 QY 230 AGGATGCTGTTACCCAGGTTAAGCTTCACTCTG 262
 DB |||||
 RESULT 3
 US-10-109-670-3
 ; Sequence 3, Application US/10109670
 ; Publication No. US20030105283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TAKESAKO, KAZUTOH et al.
 ; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
 ; FILE REFERENCE: 1422-0523P
 ; CURRENT APPLICATION NUMBER: US/10/109,670
 ; CURRENT FILING DATE: 2002-04-01
 ; NUMBER OF SEQ ID NOS: 58
 ; SEQ ID NO 3
 ; LENGTH: 728
 ; TYPE: DNA
 ; ORGANISM: Malassezia furfur
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(728)

OTHER INFORMATION: Strandedness:double-Topology:linear-Molecule Type:cDNA to mRNA
US-10-109-670-3

Query Match 2.3%; Score 84.2; DB 14; Length 728;
Best Local Similarity 71.9%; Pred. No. 1.1e-14;
Matches 110; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
QY 1305 AGCCCTGGAGCCTCCATCTCCAGGAGATCATGACCCCTTCCACACCAAGCACCATC 1364
DB 50 ATGGCTGGAGCCGTTTACTCTTAAGGAGATCATGCGTCCACACCAAGCACCACC 109
QY 1365 AGACTTATGTTAAGCGCTCAACGTCGCCGAGGAGCTACTCGGCCCTGTGGCGAAG 1424
DB 110 AGACTTATGTTAAGCGCTCAACGTCGCCGAGGAGCTACTCGTGGCGGCGGGA 169
QY 1425 AGGATGTCCTTACCAGGTTAAGCTTCACTCTG 1457
DB 170 ACAGCTGCTTAAAGCAGATCCAGCTGCAGAGTG 202

RESULT 4
US-10-044-090-836
Sequence 836, Application US/10044090
Publication No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 836
LENGTH: 972
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 010001CB1
US-10-044-090-836

Query Match 2.0%; Score 74; DB 13; Length 972;
Best Local Similarity 67.5%; Pred. No. 2.1e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCCTGGAGCCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 1366
DB 202 GCCCTGGAGCCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 261
QY 1367 ACTTATGTTAAGCGCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 1426
DB 262 GCCTAGTGAACACCTGAAGTCAACGCGAGATCATGACCTTCCACCAAGCACCATCAG 321
QY 1427 GATGTGTTACCGAGTTAAGCTTCACTCTGTAC 1460
DB 322 GATGTGTTACCGAGTATGCTTCTCAGCCTGCAC 355

RESULT 5
US-10-198-846-13503
Sequence 13503, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13503
LENGTH: 996
TYPE: DNA
ORGANISM: Homo sapiens
US-10-198-846-13503
Query Match 2.0%; Score 74; DB 14; Length 996;
Best Local Similarity 67.5%; Pred. No. 2.1e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCCTGGAGCCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 1366
DB 199 GCCCTGGAGCCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 258
QY 1367 ACTTATGTTAAGCGCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 1426
DB 259 GCCTAGTGAACAACTCAAGTCAACGCGAGGAGATCATGACCTTCCACCAAGGGA 318
QY 1427 GATGTGTTACCGAGTTAAGCTTCACTCTGTAC 1460
DB 319 GATGTGTTACCGAGTATGCTTCTCAGCCTGCAC 352

RESULT 6
US-09-954-456-1822
Sequence 1822, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patent version 3.0
SEQ ID NO 1822
LENGTH: 1026
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-1822

Query Match 2.0%; Score 74; DB 9; Length 1026;
Best Local Similarity 67.5%; Pred. No. 2.2e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1307 GCCCTGGAGCCTCCATCTCCAGGAGATCATGACCCCTTCCACCAAGCACCATCAG 1366
DB 113 GCCCTGGAGCCTCCATCTCCAGGAGATCATGACCTTCCACCAAGCACCATCAG 172

Qy	1367	ACTATGTTAA	CGCCTCA	CGCTGCGGAGAG	AGTACTGCGCGCTGTGGCAAGAG	1426
Db	173	GCCTACGTGAAC	ACCTGAACGT	CACGAGGAGA	GTACCAAGAGGCGTTGGCCAAGGA	232
Qy	1427	GATGTGCTTACCC	AGGTTAA	AGCTTCAGTCTGAC	1460	
Db	233	GATGTTACGCC	CAGATAGTCTTC	CAGCCTGCAC	266	
RESULT 7						

RESULT 7

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US-10-342-887-509
; Sequence 509, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 509
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-509

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	Query Match	2.0%	Score 74;	DB 12;	Length 1026;
	Best Local Similarity	67.5%;	Pred. No. 2.2e-11;		
	Matches 104;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0;
QY	1307	GCCTCGAGCCCTCCATCTCCRAAGGAGATCATGACCTTCACACACCAAGCAGCATCAG	1366		
Db	113	GCCTTGGAACTTCACATCAACGCGCAGATCATGCGCTGCACCACGACCAAGCACCACGCG	172		
QY	1367	ACTTATGTGTTAAACGGCCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGGCCAAAGGAG	1426		
Db	173	GCCTACGTGAACAACCTGAACGTCACCGAGGAGAGTACCAGGAGGGGTGGCCCAAGGGA	232		
QY	1427	GATGTGCTTACCGAGGTTTAACTTCAGTCTGTGTAC	1460		
Db	233	GATGTTACAGCCCGAGATAGCTCTTCAGCTCTGCAC	266		

RESULT 8

US-10-342-887-1905
; Sequence 1905, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342.887

```

; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1905
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1905

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	Query Match	2.0%;	Score 74;	DB 12;	Length 1026;
	Best Local Similarity	67.5%;	Pred. No. 2.2e-11;		
	Matches 104;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0;
Qy	1307	GCCTGAGCCCTCCATCTCCAAAGGAGATCATGCACCTTACCACACCAAGCACCATCAG	1366		
Db	113	GCCTTGAACCTCACAATCAACGGCGAGATCATGCAGCTGCACCACCAAGCACCCAGCG	172		
Qy	1367	ACTTATGTTTAAACGGCCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGCGCAAGGAG	1426		
Db	173	GCCTACGTGAACAACCTGAACGTCCCGAGGAGAGTACCAAGGAGGCTTGGCCAAAGGA	232		
Qy	1427	GATGTGTTTACCAGGTTAAGCTTCAGTCTGTATC	1460		
Db	233	GATGTTTACGCCCAGATAGCTCTTTCAGCTCTGCAC	266		

RESULT 9

```

US-09-971-429B-22
; Sequence 22, Application US/09971429B
; Publication NO. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971,429B
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239, 024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 1067
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 241107.17
US-09-971-429B-22

```

	Query Match	2.0%;	Score 74;	DB 10;	Length 1067;
	Best Local Similarity	67.5%;	Pred. No. 2.2e-11;		
	Matches 104;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0;
QY	1307	GCCTCGAGCCCTCCATCTCCAAAGAGATCATGACCCITTCACACACCAAGCACCATCAG	1366		
Db	272	GCCTGGAACTTCATCATCAACCGGCAGATCATGCGCTGCACACAGCAAGCACCAACGCG	331		
QY	1367	ACTTATGTTTAACGGCCTCAACGCTGCCGAGGAGAGTACTCGGCCGCTCTGGGCAAGGAG	1426		
Db	332	GCCTAGTGAAACAACCTGAACTCACCGAGGAGAGTACACGAGGCGCTTGGCCACGGGA	391		
QY	1427	GATGTGCTTACCGAGTTAAGTCTCAGTCTGTAC	1460		
Db	392	GATGTTACAGCCAGATAGCTCTTCAGCCTGCAC	425		

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RESULT 10
US-09-917-800A-1627
; Sequence 1627, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1627
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_017051
; US-09-917-800A-1627

Query Match          2.0%; Score 74; DB 9; Length 1492;
Best Local Similarity 67.5%; Pred. No. 2.9e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1307 GCCCTGGAGCCCTCCATCTCCAAAGGAGATCATGACCCCTTCAACCAAGCAACCATCAG 1366
    |||||
Db 177 GCGCTGGAGCCGCACATTAAACGCGCAGATCATGACCTGCACACACAGCAAGCAACCGCG 236

QY 1367 ACTTATGTTAAGCGCTCAACGCTCCGAGGAGACTACTCGCGCTGTGGGCAAGGAG 1426
    |||||
Db 237 ACCTACGTGAACAATCTGAACGTCACCGAGGAGAGTACCAAGGCGGTGGCCAAAGGA 296

QY 1427 GATGTGCTTACCAGGTTAAAGCTTCAGTCTGTAC 1460
    |||||
Db 297 GATGTACAACTCAGGTTGCTCTTTCAGCTGTGCAC 330

RESULT 11
US-10-198-846-13787
; Sequence 13787, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049

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; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13787
; LENGTH: 2825
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13787

Query Match          2.0%; Score 74; DB 14; Length 2825;
Best Local Similarity 67.5%; Pred. No. 4.7e-11;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1307 GCCCTGGAGCCCTCCATCTCCAAAGGAGATCATGACCCCTTCAACCAAGCAACCATCAG 1366
    |||||
Db 258 GCGCTGGAACTCATCATCAACGCGCAGATCATGAGCTGCACCAAGCAACCATCAGCGG 317

QY 1367 ACTTATGTTAAGCGCTCCATCTCCAAAGGAGAGCTACTCGCGCTGTGGGCAAGGAG 1426
    |||||
Db 318 GCCTACGTGAACAACCTGAACGCTCACCGAGGAGAGTACCAAGCAACCATCAGCGG 377

QY 1427 GATGTGCTTACCAGGTTAAAGCTTCAGTCTGTAC 1460
    |||||
Db 378 GATGTTACAGCCAGATAGCTCTTCAGCTGTGCAC 411

RESULT 12
US-09-993-333-11
; Sequence 11, Application US/09993333
; Patent No. US20020156040A1
; GENERAL INFORMATION:
; APPLICANT: Oberley, Larry Wayne
; APPLICANT: Weydert, Christine J.
; APPLICANT: Smith, Benjamin Barnes
; TITLE OF INVENTION: Reduction of antioxidant enzyme levels in tumor cells using antis
; TITLE OF INVENTION: oligonucleotides
; FILE REFERENCE: 875,042US1
; CURRENT APPLICATION NUMBER: US/09/993,333
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/248,328
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-993-333-11

Query Match          2.0%; Score 73; DB 9; Length 325;
Best Local Similarity 67.3%; Pred. No. 1.8e-11;
Matches 103; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1307 GCCCTGGAGCCCTCCATCTCCAAAGGAGATCATGACCCCTTCAACCAAGCAACCATCAG 1366
    |||||
Db 149 GCGCTGGAACTCATCATCAACGCGCAGATCATGAGCTGCACCAAGCAACCATCAGCGG 208

QY 1367 ACTTATGTTAAGCGCTCAACGCTCCGAGGAGAGCTACTCGCGCTGTGGGCAAGGAG 1426
    |||||
Db 209 GCGCTACGTGAACAACCTGAACGTCACCGAGGAGAGTACCAAGGCGGTGGCCAAAGGA 268

QY 1427 GATGTGCTTACCAGGTTAAAGCTTCAGTCTGTA 1459
    |||||
Db 269 GATGTTACAGCCAGATAGCTCTTCAGCTGTGCA 301

RESULT 13
US-09-960-352-14744
; Sequence 14744, Application US/09960352
; Patent No. US20020137139A1

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; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14744
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 63-LIB3057-022-Q1-K1-H4
US-09-960-352-14744

Query Match      2.0%; Score 72.6; DB 9; Length 424;
Best Local Similarity 67.5%; Pred. No. 3e-11;
Matches 102; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCTTCACACACCAAGCACCATCAG 1366
Db 157 GCCTGGAGCCGCACATCAACGCGCAGATCATGCGTGCACACAGCAAGCACCACGCG 216
QY 1367 ACTATGTTAAACGGCTCAACGCTGCCGAGGAGAGCTACTCGCGCTGTGGCAAGGAG 1426
Db 217 GCCTAGTGNACCTCAACGCTGCCGAGGAGAGTACCGGAGGCGCTGGAGAAGGGT 276
QY 1427 GATGCTTACCAGGTTAAGCTTCAAGTCTG 1457
Db 277 GATGTTACAGCTCAGATAGCTCTGCAGCCTG 307

RESULT 14
US-10-044-090-709
; Sequence 709, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 709
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 241107.13
US-10-044-090-709

Query Match      2.0%; Score 71; DB 13; Length 2208;
Best Local Similarity 66.9%; Pred. No. 3.4e-10;
Matches 101; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1310 CTGGAGCCCTCCATCTCCAGGAGATCATGACCTTCACACACCAAGCACCATCAGACT 1369
Db 117 CTGGAACCTCAGATCAACGCGCAGATCATGCGTGCACACAGCAAGCACCACCGCGCC 176
QY 1370 TATGTTAAGCGCTCAACGCTGCCGAGGAGAGTACTCGGCGCTGTGGCAAGGAGGAT 1429
Db 177 TAGCTGAACAACCTCAACGCTGCCGAGGAGAGTACCAGAGGCGCTTGGCCCAAGGAGAT 236
QY 1430 GTGCTTACCCAGGTTAAGCTTCAAGTCTGCTAC 1460
Db 237 GTTACAGCCCATAGTAGCTCTTCAGCCTGCAC 267

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RESULT 15
US-09-727-855B-6
; Sequence 6, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
; FILE OF INVENTION: MATERIALS THEREOF
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Phaffia rhodozyma
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(594)
; OTHER INFORMATION:
US-09-727-855B-6

Query Match      1.9%; Score 69.8; DB 9; Length 597;
Best Local Similarity 73.8%; Pred. No. 2.9e-10;
Matches 89; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2389 AGATCTGGGAGCAGCTTTCTACCTTCAGTACAAAGAACGTCAAAGCCTGACTATCTGCTG 2448
Db 473 ACATCTGGGAGCAGCTTTCTACCTTCAGTACAAAGAACGTCAAAGCCTGACTATCTGCTG 532
QY 2449 CTGTTTGGTCCGTTATCAACTACAAAGGAGGAGGCGCGATTGCGAGGCTGCTCTTAAG 2508
Db 533 CTTTCTGGAACGCTCTGCAACTTTGCTGAGGCTCAGCGAAGTTTGATGCTGCTGCTCAAG 592
QY 2509 C 2509
Db 593 C 593

Search completed: April 1, 2004, 14:10:44
Job time : 1277.68 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 12:35:05 ; Search time 14031.5 Seconds
(without alignments)
11219.210 Million cell updates/sec

Title: US-09-727-855B-1

Perfect score: 3632

Sequence: 1 tctgttgataatcttcta.....aagagcttgacattgttag 3632

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3	151.4	4.2	669	6	AX128479	AX128479 Sequence
4	151.4	4.2	669	6	BD015713	BD015713 Recombina
5	94.8	2.6	7218	6	I66494	I66494 Sequence 14
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ALIGNMENTS

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ACCESSION	AX128476.1	GI:14134943				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
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	Xanthophyllomyces dendrorhous					
	Eukaryota; Fungi; Basidiomycota; Hymenomycetes;					
	Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;					
	Cystofilobasidiales; Xanthophyllomyces.					
REFERENCE						
AUTHORS	Hoshino,T., Ojima,K. and Setoguchi,Y.					
TITLE	Recombinant production of carotenoids, particularly astaxanthin					

Pred. No. is the number of results predicted by chance to have a

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LOCUS	KEYWORDS	
DEFINITION	SOURCE	
	ORGANISM	

TITLE	JOURNAL	COMMENT	Recombination production of carotenoids, in particular, astaxanthin	
Patent: JP 2001190294-A	1 17-JUL-2001;	F HOFFMANN LA ROCHE AG		
OS	Phaffia rhodozyma			
PN	JP 2001190294-A/1			
PD	17-JUL-2001			
PF	01-DEC-2000	JP 2000367099		
PR	01-DEC-1999	EP 99123821.3		
PI	TATSUO HOSHINO, KAZUYUKI OJIMA, YUTAKA SETO, GUCHI PC			
CI	C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12P23/00, C12O1/68// PC			
CL	C12P23/00, C12R1/01, (C12P23/00, C12R1/18), (C12P23/00, C12R1/20), PC			
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RESULT 7

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Matches 96; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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VERSION      Z18857.1 GI:288504
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SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
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AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE      Hallowell, R.A., Mullenbach, G.T., Stempien, M.M. and Bell, G.I.
MEDLINE      Sequence of a cDNA coding for mouse manganese superoxide dismutase
PUBMED      Nucleic Acids Res. 14 (23), 9539 (1986)
87091590
3797253

REFERENCE      2 (bases 1 to 779)
AUTHORS      Sun, Y., Hegamyer, G. and Colburn, N.H.
JOURNAL      Sequence of manganese superoxide dismutase-encoding cDNAs from
TITLE      multiple mouse organs
MEDLINE      Gene 131 (2), 301-302 (1993)
PUBMED      84010326
8406027

REFERENCE      3 (bases 1 to 779)
AUTHORS      Sun, Y.
JOURNAL      Direct Submission
TITLE      Submitted (25-NOV-1992) Sun Y., FCRDC, CBS, LVC, P.O. Box B,
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QY 1367 ACTTATGTTTAAAGCGCTCAACGCTGCCGAGGAGAGTACTCGGCCGCTGTGGGCAAGAG 1426
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Db 264 GATGTTACAACCTCAGGTCGCTCTTCAGCCTGCAC 297
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RESULT 10
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LOCUS      Mouse mRNA for manganese superoxide dismutase (MnsOD).
ACCESSION      X04972
VERSION      X04972.1 GI:53449
KEYWORDS      manganese superoxide dismutase; superoxide dismutase.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 897)
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL      Hallowell, R.A., Mullenbach, G.T., Stempien, M.M. and Bell, G.I.
TITLE      Sequence of a cDNA coding for mouse manganese superoxide dismutase
MEDLINE      Nucleic Acids Res. 14 (23), 9539 (1986)
PUBMED      87091590
3797253

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LOCUS AB087277 600 bp mRNA linear PRI 04-OCT-2002
DEFINITION Macaca fuscata mRNA for Mn-superoxide dismutase, complete cds.
ACCESSION AB087277
VERSION AB087277.1 GI:23503531
KEYWORDS
SOURCE Macaca fuscata (Japanese macaque)
ORGANISM
Macaca fuscata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.

REFERENCE
1 Fukuhara,R., Tezuka,T. and Kageyama,T.
Structure, molecular evolution, and gene expression of primate
superoxide dismutases
Gene 296, 99-109 (2002)
JOURNAL
AB087277
AUTHORS Fukuhara,R. and Kageyama,T.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2002) Ryoji Fukuhara, Primate Research Institute,
Kyoto University, Center for Human Evolution Modeling Research;
Kanrin, Inuyama, Aichi 484-8506, Japan
(E-mail:fukuhara@pri.kyoto-u.ac.jp, Tel:81-568-63-0578,
Fax:81-568-63-0085)
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Db 100 GCCTACGTGAACAACCTGAACCTTACCGAGGAGAGTACCAGAGCGCTTGCCCAAGGA 159

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Db 160 GATGTTACAGCCCGCATAGTCTCTTCAGCCTGCAC 193

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LOCUS AB087278 600 bp mRNA linear PRI 04-OCT-2002
DEFINITION Macaca fascicularis mRNA for Mn-superoxide dismutase, complete cds.
ACCESSION AB087278
VERSION AB087278.1 GI:23503533
KEYWORDS
SOURCE Macaca fascicularis (crab-eating macaque)
ORGANISM
Macaca fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.

REFERENCE
1 Fukuhara,R., Tezuka,T. and Kageyama,T.
Structure, molecular evolution, and gene expression of primate
superoxide dismutases
Gene 296, 99-109 (2002)
JOURNAL
AB087278
AUTHORS Fukuhara,R. and Kageyama,T.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2002) Ryoji Fukuhara, Primate Research Institute,
Kyoto University, Center for Human Evolution Modeling Research;
Kanrin, Inuyama, Aichi 484-8506, Japan
(E-mail:fukuhara@pri.kyoto-u.ac.jp, Tel:81-568-63-0578,
Fax:81-568-63-0085)
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Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.

REFERENCE
1 Fukuhara,R., Tezuka,T. and Kageyama,T.
Structure, molecular evolution, and gene expression of primate
superoxide dismutases
Gene 296, 99-109 (2002)
JOURNAL
AB087277
AUTHORS Fukuhara,R. and Kageyama,T.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2002) Ryoji Fukuhara, Primate Research Institute,
Kyoto University, Center for Human Evolution Modeling Research;
Kanrin, Inuyama, Aichi 484-8506, Japan
(E-mail:fukuhara@pri.kyoto-u.ac.jp, Tel:81-568-63-0578,
Fax:81-568-63-0085)
Location/Qualifiers
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ACCESSION AB087279
VERSION AB087279.1 GI:23503535
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Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.

REFERENCE
1 Fukuhara,R., Tezuka,T. and Kageyama,T.
Structure, molecular evolution, and gene expression of primate
superoxide dismutases
Gene 296, 99-109 (2002)
JOURNAL
AB087279
AUTHORS Fukuhara,R. and Kageyama,T.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2002) Ryoji Fukuhara, Primate Research Institute,
Kyoto University, Center for Human Evolution Modeling Research;
Kanrin, Inuyama, Aichi 484-8506, Japan
(E-mail:fukuhara@pri.kyoto-u.ac.jp, Tel:81-568-63-0578,
Fax:81-568-63-0085)
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1. .600
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QY 1427 GATGTGCTTACCCAGGTTAAGCTTCACTCTGTAC 1460
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  ACCESSION AB087276
  VERSION AB087276.1 GI:23503529
  KEYWORDS
  SOURCE
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    Hylobates lar
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    Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
  REFERENCE
    1 Fukuhara,R., Tezuka,T. and Kageyama,T.
      Structure, molecular evolution, and gene expression of primate
      superoxide dismutases
      Gene 296, 99-109 (2002)
  JOURNAL
    2 (bases 1 to 600)
  REFERENCE
    Fukuhara,R. and Kageyama,T.
  AUTHORS
    Direct Submission
  TITLE
    Submitted (02-JUL-2002) Ryoji Fukuhara, Primate Research Institute,
    Kyoto University, Center for Human Evolution Modeling Research;
    Kanrin, Inuyama, Aichi 484-8506, Japan
    (E-mail:fukuhara@pri.kyoto-u.ac.jp, Tel:81-568-63-0578,
    Fax:81-568-63-0085)
  JOURNAL
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 13:12:34 ; Search time 9327 Seconds
(without alignments)
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Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10	78.8	2.2	372	13	BY300950
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17	78.8	2.2	710	10	BF607468
18	78.8	2.2	730	12	BI904486
19	78.8	2.2	995	14	CF583893
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24	77.4	2.1	679	14	CA376311
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33	76.2	2.1	336	13	BY789405
34	76.2	2.1	416	13	BY273152
35	75.8	2.1	475	12	BJ490136
36	75.8	2.1	604	12	BJ491899
37	75.8	2.1	640	9	AU170704
38	75.6	2.1	643	9	AU169164
39	75.6	2.1	332	13	BY334907
40	75.6	2.1	357	13	BY041846
41	75.6	2.1	358	13	BY085746
42	75.6	2.1	358	13	BY163920
43	75.6	2.1	368	13	BY072632
44	75.6	2.1	370	13	BY168947
45	75.6	2.1	372	13	BY042164

ALIGNMENTS

RESULT 1
CF192114
LOCUS
DEFINITION
13917j2.r1 Cryptococcus neoformans strain BJ501 Cryptococcus
neoformans var. neoformans cDNA clone l3917j2 5', mRNA sequence.
ACCESSION
CF192114
VERSION
CF192114.1 GI:33513983
KEYWORDS
EST.
SOURCE
Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
ORGANISM
Cryptococcus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.
REFERENCE
1 (bases 1 to 333)
AUTHORS
Kupfer,D.M., Drabenstot,S.D., Buchanan,K.L., Lai,H., Dyer,D.W.,
Roe,B.A. and Murphy,J.W.
TITLE
Comparison of highly conserved intronic and exonic elements
associated with splicing among five diverse fungal organisms
JOURNAL
Unpublished (2003)
COMMENT
Other_ESTs: l3917j2.f1
Contact: Murphy, JW
Department of Microbiology and Immunology
University of Oklahoma Health Sciences Center
Oklahoma City, OK 73190, USA
Tel: 405-271-2133 ex2133
Email: juneann-murphy@ouhsc.edu

BY327331 BY327331
BQ086753 ih89d09.y
BY315073 BY315073
BB856053 BB856053
BY310981 BY310981
BY300950 BY300950
CB274248 mai90f09.
BG04894 0273-74 M
CA889637 B0154B09-
BI713308 ic86g07.y
BU743935 mai50e03
BI526549 602924986
BF607468 MW1_00041
BI904486 603168211
CF583893 AGENCOURT
CB589814 AGENCOURT
CA352127 623328 NC
CA387190 669009 NC
EX076652 EX076652
CA376311 654638 NC
CA375800 653967 NC
EX855859 EX855859
BY173533 BY173533
BY298840 BY298840
BQ102079 ih86c08.y
BY303463 BY303463
CD467777 LeukoS1_6
CA765001 AF53-RpF
BY789405 BY789405
BY273152 BY273152
BJ490136 BJ490136
BJ491899 BJ491899
AU170704 AU170704
AU169164 AU169164
BY334907 BY334907
BY041846 BY041846
BY085746 BY085746
BY163920 BY163920
BY072632 BY072632
BY168947 BY168947
BY042164 BY042164

This clone is available from the Fungal Genetics Stock Center,
Phone 913-588-7044, <http://www.fgsc.net/> Contact Dr. Bruce Roe
(broe@ou.edu, www.genome.ou.edu) for sequencing questions Contact
Dr. Juneann Murphy (juneann-murphy@ouhsc.edu) for library
information.

Seq primer: T3
High quality sequence stop: 327.

FEATURES

Location/Qualifiers

source

1. .333
/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="B3501"
/db_xref="taxon:40410"
/clone="j5k07j2"
/lab_host="E. coli strain SOLR"
/clone_lib="Cryptococcus neoformans strain B3501"
/note="Vector: pBluescript sk-; Site_1: EcoRI at 5' end of
cDNA insert; Site_2: XhoI at 3' end of cDNA insert"

ORIGIN

Query Match 2.3%; Score 85; DB 14; Length 333;
Best Local Similarity 77.4%; Pred. No. le-08;
Matches 103; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2389 AGATCTGGAGCAGCGTTTCTACCTTCAGTACAGAGCGTCAAGCGTCACTATCTCGCTG 2448
Db |||||
200 ACATCTGGAGCAGCGTTTCTATCTCCAGTACAGAGCGTCAAGCGTCACTATCTCAATG 259
|||
Qy 2449 CTGTTTGGTCCGTTTATCAACTACAGGAGGAGGCGCCGATTCGAGGCTGCTCTTAAG 2508
Db |||||
260 CCACTCGAATGTTATCAACTACGAGGAGGCGGAAAGTCGTCTCAAGGCTGCTCAGTAAG 319
|||
Qy 2509 CGGACGAAAAGT 2521
Db |||||
320 CTTTATGAACAAT 332
|||

RESULT 2

CF186948/c 388 bp mRNA linear EST 08-AUG-2003
LOCUS j5k07j2.f1 Cryptococcus neoformans strain B3501 Cryptococcus
neoformans var. neoformans cDNA clone j5k07j2 3', mRNA sequence.

ACCESSION

CF186948

VERSION

CF186948.1 GI:33508916

KEYWORDS

EST.

SOURCE

Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
var. neoformans)
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
Filobasidiella.

REFERENCE

1 (bases 1 to 388)
Kupfer, D.M., Drabenstot, S.D., Buchanan, K.L., Lai, H., Dyer, D.W.,
Roe, B.A. and Murphy, J.W.

AUTHORS

Comparison of highly conserved intronic and exonic elements

TITLE

Associated with splicing among five diverse fungal organisms

JOURNAL

Unpublished (2003)

COMMENT

Other ESTs: j5k07j2.r1
Contact: Murphy, JW
Department of Microbiology and Immunology
University of Oklahoma Health Sciences Center
Oklahoma City, OK 73190, USA
Tel: 405-271-2133 ex2133
Email: juneann-murphy@ouhsc.edu
This clone is available from the Fungal Genetics Stock Center,
Phone 913-588-7044, <http://www.fgsc.net/> Contact Dr. Bruce Roe
(broe@ou.edu, www.genome.ou.edu) for sequencing questions Contact
Dr. Juneann Murphy (juneann-murphy@ouhsc.edu) for library
information.

Seq primer: M13-20

High quality sequence stop: 379.

FEATURES

Location/Qualifiers

source

1. .388

/organism="Cryptococcus neoformans var. neoformans"
/mol_type="mRNA"
/strain="B3501"
/db_xref="taxon:40410"
/clone="j5k07j2"
/lab_host="E. coli strain SOLR"
/clone_lib="Cryptococcus neoformans strain B3501"
/note="Vector: pBluescript sk-; Site_1: EcoRI at 5' end of
cDNA insert; Site_2: XhoI at 3' end of cDNA insert"

ORIGIN

Query Match 2.3%; Score 85; DB 14; Length 388;
Best Local Similarity 77.4%; Pred. No. le-08;
Matches 103; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2389 AGATCTGGAGCAGCGTTTCTACCTTCAGTACAGAGCGTCAAGCGTCACTATCTCGCTG 2448
Db |||||
200 ACATCTGGAGCAGCGTTTCTATCTCCAGTACAGAGCGTCAAGCGTCACTATCTCAATG 141
|||
Qy 2449 CTGTTTGGTCCGTTTATCAACTACAGGAGGAGGCGCCGATTCGAGGCTGCTCTTAAG 2508
Db |||||
140 CCACTCGAATGTTATCAACTACGAGGAGGCGGAAAGTCGTCTCAAGGCTGCTCAGTAAG 81
|||
Qy 2509 CGGACGAAAAGT 2521
Db |||||
80 CTTTATGAACAAT 68
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RESULT 3

CF192113/c

LOCUS 400 bp mRNA linear EST 08-AUG-2003

DEFINITION 13g17j2.f1 Cryptococcus neoformans strain B3501 Cryptococcus

neoformans var. neoformans cDNA clone 13g17j2 3', mRNA sequence.

ACCESSION CF192113

VERSION CF192113.1

KEYWORDS GI:33513982

SOURCE EST.

Cryptococcus neoformans var. neoformans (Filobasidiella neoformans

var. neoformans)

Cryptococcus neoformans var. neoformans

Eukaryota; Fungi; Basidiomycota; Hymenomycetes;

Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;

Filobasidiella.

1 (bases 1 to 400)

Roe, B.A. and Murphy, J.W.

Comparison of highly conserved intronic and exonic elements

associated with splicing among five diverse fungal organisms

Unpublished (2003)

Other ESTs: 13g17j2.r1

Contact: Murphy, JW

Department of Microbiology and Immunology

University of Oklahoma Health Sciences Center

Oklahoma City, OK 73190, USA

Tel: 405-271-2133 ex2133

Email: juneann-murphy@ouhsc.edu

This clone is available from the Fungal Genetics Stock Center,

Phone 913-588-7044, <http://www.fgsc.net/> Contact Dr. Bruce Roe

(broe@ou.edu, www.genome.ou.edu) for sequencing questions Contact

Dr. Juneann Murphy (juneann-murphy@ouhsc.edu) for library

information.

Seq primer: M13-20.

Location/Qualifiers

source

1. .400

/organism="Cryptococcus neoformans var. neoformans"

/mol_type="mRNA"

/strain="B3501"

/db_xref="taxon:40410"

/clone="13g17j2"

/lab_host="E. coli strain SOLR"

/clone_lib="Cryptococcus neoformans strain B3501"

/note="Vector: pBluescript sk-; Site_1: EcoRI at 5' end of

cDNA insert; Site_2: XhoI at 3' end of cDNA insert"

ORIGIN

100

Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K., Gough S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Jarvis E.D., Kanai A., Kustwisch S., Hirokawa N., Jackson I.J., King B.L., Konagaya A., Kwaj J.H., Kawasawa Y., Kedzierzki R.M., Lyons P.A., Maglott D.R., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais K., Mochizuki L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner J., Wallestedt C., Wang Y., Watanabe Y., Wells L., Wilming L.G., Wynshaw-Boris A., Yangigawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E. and Hayashizaki Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

Contact: Yoshihide Hayashizaki

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp

URL: http://genome.gsc.riken.go.jp/

Aizawa K., Akimura T., Arakawa T., Carninci P., Fukuda S., Hayashizaki Y., Imotani K., Ishii Y., Itoh M., Kawai J., Konno H., Miyazaki A., Murata M., Nakamura M., Nomura K., Numazaki R., Ohno M., Sakai K., Sakazume N., Sasaki D., Sato K., Shibata K., Shiraki T., Tagami M., Waki K., Watahiki A., Muramatsu M. and Hayashizaki Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a non-redundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Location/Qualifiers

1. .353

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="L030041H17"

/cell_type="synovial fibroblasts"

/clone.lib="RIKEN full-length enriched, synovial fibroblasts"

ORIGIN

Query Match 2.2%; Score 78.8; DB 13; Length 353;

Best Local Similarity 69.5%; Pred. No. 2.8e-07;

Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

1307 GCCTGTGAGCCCTTCATCTCCAGGAGATCATGACCTTCACACACCAAGCACCATCAG 1366

177 GCCTGTGAGCCACATTAAGCGCAGATCATGCTGCACACGAGGCTCTGGCAAGGGA 236

1367 ACTATGTTTACGGCTCAAGCTGCGGAGGAGAGTACTCGGCCGTGTGGCAAGGAG 1426

237 GCCTGTGAGCAACCTCAAGCCACCGAGGAGAGTACCAAGGCTCTGGCAAGGGA 296

1427 GATGCTGTTACCCAGGTTAAGCTTCAGTCTGTAC 1460

297 GATGCTTACACTCAGGTCGCTTTCAGCGTGCAC 330

RESULT 6

LOCUS BQ086753 359 bp mRNA linear EST 05-APR-2002

DEFINITION BQ086753 ih89d09.y1 Melton Mouse E16 5 Pancreas Library 2 M16B2 Mus musculus cDNA clone IMAGE:5939369 5' similar to SW:SODM MOUSE P09671 SUPEROXIDE DISMUTASE [NM], MITOCHONDRIAL PRECURSOR ; , mRNA sequence.

ACCESSION BQ086753

VERSION BQ086753.1 GI:20045957

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 359)

AUTHORS Melton D., Brown J., Kenty G., Permutt A., Lee C., Kaestner K., Lemiska L., Searce M., Brestelli J., Gradwohl G., Clifton S., Hillier L., Marra M., Pape D., Wylie T., Martin J., Blistain A., Schmitt A., Theising B., Ritter R., Ronko I., Bennett J., Cardenas M., Gibbons M., McCann R., Cole R., Tsagarisshvili R., Williams T., Jackson Y. and Bowers Y.

TITLE Endocrine Pancreas Consortium

JOURNAL Unpublished (2000)

COMMENT Other ESTs: ih89d09.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@bichp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by Washington University Genome Sequencing Center This clone is available royalty-free through LLNL; please contact the IMAGE consortium (infoimage.llnl.gov) for further information

Seq primer: -40RP from Gibco.

Location/Qualifiers

1. .359

/organism="Mus musculus"

/mol_type="mRNA"

/strain="ICR"

/db_xref="taxon:10090"

/clone="IMAGE:5939369"

/sex="Both"

/tissue type="Total pancreas"

/dev stage="Embryonic day 16.5"

/lab_host="TOP10"

/clone.lib="Melton Mouse E16 5 Pancreas Library 2 M16B2"

/note="Organ: Pancreas; Vector: pBluescript II SK; Site: 1: NotI; Site 2: SalI; Library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.06kb. Primary library,

FEATURES

source

unamplified."

ORIGIN

Query Match 2.2%; Score 78.8; DB 13; Length 359;
 Best Local Similarity 69.5%; Pred. No. 2.8e-07;
 Matches 107; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1307 GCCTGGAGGCGCTCATCTCCAAAGAGATCATGACCTTCACCAAGCACCACATCAG 1366
 |||||
 Db 104 GCGCTGGAGCCACATTAACGCGCAGATCATGCGCTGACCAAGCACCACATCGG 163
 |||||

QY 1367 ACTTATGTTACGCGCTCAAGCGTCCGAGAGAGCTACTCGGCGCTGTGGCAAGGAG 1426
 |||||
 Db 164 GCCTACGTGAACACCTCAACGCCACGAGGAGAAGTACCACGAGGCTCTGCCCAAGGGA 223
 |||||

QY 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
 |||||

Db 224 GATGTACACTCAGTGGCTCTTCAGCCTGCAC 257
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RESULT 7
 BY315073 359 bp mRNA linear EST 11-DEC-2002
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 359)

REFERENCE

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikiado, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
 Kiyosawa, H., Yagi, K., Tonari, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V.,
 Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konagaya, A.,
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Sempke, C.A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
 Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, K., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE

Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 12466851

COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.

Tissues were provided by Takashi Ishikawa (Department of Surgery
 2 Yokohama City University 3-9 Fukuura, Kanazawa-Ku, Yokohama
 236-0004 Japan) whose assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

source

1. 359
 /location="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="I420017L02"
 /cell_type="osteoclast-like cell"
 /clone_lib="RIKEN full-length enriched, osteoclast-like
 cell"

ORIGIN

Query Match 2.2%; Score 78.8; DB 13; Length 359;
 Best Local Similarity 69.5%; Pred. No. 2.8e-07;
 Matches 107; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1307 GCCTGGAGGCGCTCATCTCCAAAGAGATCATGACCTTCACCAAGCACCACATCAG 1366
 |||||
 Db 174 GCGCTGGAGCCACATTAACGCGCAGATCATGACCTTCACCAAGCACCACATCGG 233
 |||||

QY 1367 ACTTATGTTACGCGCTCAAGCGTCCGAGAGAGCTACTCGGCGCTGTGGCAAGGAG 1426
 |||||
 Db 234 GCTTACGTGAACAACTCAACCTCAACGCCACGAGGAGATACCAAGGCTCTGCCCAAGGGA 293
 |||||

QY 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
 |||||

Db 294 GATGTACACTCAGTGGCTCTTCAGCCTGCAC 327
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RESULT 8

BB856053

LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE

AUTHORS

BB856053 362 bp mRNA linear EST 26-NOV-2001
 CDNA clone G370031F20 5', mRNA sequence.
 BB856053
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 362)
 Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
 Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K.,
 Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,

KEYWORDS

SOURCE
ORGANISMREFERENCE
AUTHORS

BST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 363)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schoenbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,

Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,

Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,

Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Jarvis, E. D., Kanai, A.,

Gustincich, S., Hirokawa, N., Jackson, I. J., King, B. L., Konagaya, A.,

Kawai, H., Kawasawa, Y., Kedzieriski, R. M., King, P. A., Maglott, D. R.,

Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Nagashima, T.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Pesole, G.,

Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S.,

Ravasi, T., Reed, J. C., Reid, J. J., Reid, J. J., Ring, B. Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,

Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

12466851

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Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp/

URL: http://genome.gsc.riken.go.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watanishi, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in Riken.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Tissues were provided by Takashi Ishikawa (Department of Surgery

2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama

236-0004 Japan) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Nomura, K., Numasaki, R.,

Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N.,

Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akaira, S.,

Tanaka, T., Tomaru, A., Toya, T., Watanishi, A., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.

2001)

Unpublished (2001)

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The Institute of Physical and Chemical Research (RIKEN)

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Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp/

URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watanishi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,

Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.

and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

e mouse tissues.

Location/Qualifiers

1..362

/organism="Mus musculus"

/mol_type="mRNA"

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Query Match 2.2%; Score 78.8; DB 10; Length 362;

Best Local Similarity 69.5%; Pred. No. 2.8e-07;

Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1307 GCGCTGGAGCCCTCCATCTCCAGGAGATCATGACCTTTCCACACCAAGCACCATCTAG 1366

Db 198 GCGCTGGAGCCACACATTAAACGCGAGATCATGACCTGCACACAGCAAGCACCATGCG 257

QY 1367 ACTTATGTTAAAGCGCTTAACGCTGCCGAGGAGAGTACTCGGCCCTGTGGCCAGGAG 1426

Db 258 GCGTACGTGAACAACCTCAACGCCACCGAGGAGAGTACCAACGAGCTCTGGCCAGGGA 317

QY 1427 GATGCTCTTACCAGGTTAAGCTTCACTCTGTAC 1460

Db 318 GATGTTTACAACTCAGGTCGCTCTTTCAGCTTCAC 351

RESULT 9

BY310981

LOCUS 363 bp mRNA linear EST 11-DEC-2002

DEFINITION BY310981 RIKEN full-length enriched, stroma cell Mus musculus cDNA

clone I320017112 5', mRNA sequence.

ACCESSION BY310981

VERSION BY310981.1 GI:26501318

further details.
 Location/Qualifiers
 1. 363
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Query Match 2.2%; Score 78.8; DB 13; Length 363;
 Best Local Similarity 69.5%; Pred. No. 2.8e-07;
 Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCATCTCCAAAGGATCATGACCTTACACACACAGCACCATCAG 1366
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BY300950 372 bp mRNA linear EST 11-DEC-2002
 BY300950 RIKEN full-length enriched, 14.5 days embryo RP+/
 Rathke's pouches Mus musculus cDNA clone K720012M21 5', mRNA
 sequence.
 BY300950
 BY300950.1 GI:26491287
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 372)
 Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
 Nikaide,I., Osato,N., Saito,R., Suzuki,H., Yamana,I.,
 Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
 Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
 Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
 Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
 Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
 Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
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 Hayatsu,N., Harozane-Kishikawa,T., Konno,H., Nakamura,M.,
 Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
 Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
 Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
 Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
 Rogers,J., Birney,E. and Hayashizaki,Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

RESULT 10
 BY300950
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

MEDLINE PUBMED COMMENT

22354683
 12466851
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
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 The Institute of Physical and Chemical Research (RIKEN)
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 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
 Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
 Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
 Ono,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
 Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
 Hayashizaki,Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Michelle Brinkmeier and Sally Camper (Dept.
 Human Genetics University of Michigan Medical School 4301
 MSRB 3 1500 W. Medical Center Dr. Ann Arbor, MI 48109-0638 USA)
 whose assistance we gratefully acknowledge.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES source

1. 372
 /organism="Mus musculus"
 /mol_type="mRNA"
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Query Match 2.2%; Score 78.8; DB 13; Length 372;
 Best Local Similarity 69.5%; Pred. No. 2.8e-07;
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QY 1307 GCCTGGAGCCCTCATCTCCAAAGGATCATGACCTTACACACACAGCACCATCAG 1366
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 QY 1427 GATGTGTTACCGAGTTAAGCTTCAGTCTGTAC 1460
 Db 127 GATGTTACAACCTCAGGTGCGCTCTTCAGCTGCAC 160

RESULT 11 CB274248 LOCUS DEFINITION

CB274248 467 bp mRNA linear EST 24-FEB-2003
 ma190f09.yl McCarrey Eddy round spermatid Mus musculus cDNA clone
 IMAGE:6448769 5' similar to SW:SODM_MOUSE P09671 SUPEROXIDE

240 GATGTTACAACTCAGGTCGCTCTTCAGCCTGCAC 273

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AUTHORS	511 bp	linear	EST 20-DEC-2001
TITLE	511 bp	linear	EST 20-DEC-2001
JOURNAL	511 bp	linear	EST 20-DEC-2001
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AUTHORS	566 bp	linear	EST 20-DEC-2002
TITLE	566 bp	linear	EST 20-DEC-2002

JOURNAL
COMMENT

CDNA Library (Long)
Unpublished (2002)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@nigun.grc.nia.nih.gov
Plate: B0154 row: B column: 09
Seq primer: -21M13 Reverse
High quality sequence stop: 566
POLYA-No.

FEATURES
source

Location/Qualifiers
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/clone_lib="NIA Mouse Neural Stem Cell (Differentiated)
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/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001)). [PMID: 11544199]. Total RNAs were
obtained from Dr. Angelo L. Vescovi (Institute for Stem
Cell Research, Italy). Double-stranded cDNAs were
synthesized with an Oligo(dT) primer [Invitrogen:
5'-pGACTAGTCTAGATCGAGCGCGCCCTTTTCTTTT-3'] from
2.0 microgram of total RNA, treated with 14 DNA
polymerase, and purified by ethanol-precipitation. The
cDNAs were ligated to lone-linker LL-Sal4, purified by
phenol/chloroform, and separated from free linkers by
Centricon 100. Then, the cDNAs were amplified by
long-range high fidelity PCR using Ex-Taq polymerase
(Takara) with a primer Sal4-S. The products were purified
by phenol/chloroform and Centricon 100. The cDNAs were
digested with SalI and NotI enzymes and cloned into
SalI/NotI site of pSPORT1 plasmid vector. The DH10B E.
coli host was transformed with the ligation mixture by the
standard chemical method. The average insert size is about
3.2 kb. The library was constructed by Yulan Piao."

ORIGIN

Query Match 2.2%; Score 78.8; DB 14; Length 566;
Best Local Similarity 69.5%; Pred. No. 2.8e-07;
Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCTTCACACACCAAGCACCATCAG 1366
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sequence.
BI713308
ACCESSION

BI713308.1 GI:15689003
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 580)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearc, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wyllie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: ic86g07.xl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
MGI:1947051 This sequence now available from the IMAGE consortium,
for clone orders contact: info@image.llnl.gov
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High quality sequence stop: 413.
Location/Qualifiers
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/sex="Both for embryonic & newborn, male for adult and
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NI-MMS1"
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libraries representing E10.5/12.5 pancreatic bud, E16.5
pancreas, newborn pancreas, adult pancreas, and adult
islets of Langerhans were separately constructed using
Superscript Plasmid Library kit (Life Technologies). cDNA
was made by oligo-dT priming and size-selected by column
fractionation. Libraries were amplified once on solid
support and plasmid DNA from each library was prepared
and mixed in equal amounts. The mixed library DNA was
normalized by method #4 from Bonaldo, Lennon, and Soares
1996 Genome Research 6:791-806; 0.5 microgram
single-stranded mixed library plasmid DNA was mixed with
5 micrograms PCR product representing mixed library
inserts and hybridized to an EcoT of 6. Single-stranded
(unhybridized) plasmids were isolated by hydroxyapatite
chromatography and used to make this library."

ORIGIN

Query Match 2.2%; Score 78.8; DB 12; Length 580;
Best Local Similarity 69.5%; Pred. No. 2.8e-07;
Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAGGAGATCATGACCTTCACACCAAGCACCATCAG 1366
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Db 110 GCGCTGGAGCCACATTAACGCGCAGATCATGCGCTGCACACCAAGCACCATGCG 169
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QY 1367 ACTTATGTTAACGGCTCAACGCTGCCGAGGAGAGTACTCGCGCTGTGGCAGGAG 1426
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RESULT 15
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 LOCUS mai50603.v1 McCarrey Eddy round spermatid Mus musculus cDNA clone
 DEFINITION IMAGE:6449477 5', similar to SW:SDM MOUSE P09671 SUPEROXIDE
 DISMUTASE [NM], MITOCHONDRIAL PRECURSOR ;, mRNA sequence.

ACCESSION BU743935
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 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 589)
 McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,
 Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M.,
 Ritter, E., Tsagarelshvili, R., Ronko, I., Maguire, L., Kennedy, S.,
 Bennett, J., Waterston, R. and Wilson, R.

TITLE NIEHS Mouse
 JOURNAL Unpublished (2002)
 COMMENT Contact: McCarrey/Eddy NIEHS Mouse
 NIEHS Mouse
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:2093789
 Seq primer: -40RP from Gibco
 High quality sequence stop: 428.

FEATURES
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 1..589
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /clone="IMAGE:6449477"
 /sex="male"
 /tissue type="round spermatids, pooled from multiple mice"
 /dev stage="60 day"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="McCarrey Eddy round spermatid"
 /note="Organ: testis; Vector: pBluescript SK+
 (Stratagene); Site 1: XhoII; Site 2: EcoRI; cDNA oligo
 dt-primed [5'-(GA)10-ACTAGTCTCGAGTTTCTTTT-3'] and
 directionally cloned using 5' linkers 5'-AATTCGCAAGGAG-3',
 and 5'-CTCGTGGCG-3'. Size selection of >400bp material
 gives average insert size ranging from 1-2 kb. Library was
 mass excised (from lambda-UniZAP-XR) and resulting
 single-stranded phagemids were prepped and transformed
 into DH10B. Library contains 98.5% recombinants.
 References: J. Androl. 20:635-639 and Gene 25:263-269.
 Library constructed and donated by J. McCarrey, Ph.D.
 (Southwest Foundation for Biomedical Research, Dept. of
 Genetics); excision done by E.M. Eddy, Ph.D. (National
 Institutes of Health, National Institute of Environmental
 Health Sciences). Original lambda-based library is
 available through ATCC, catalog #63423."

ORIGIN

Query Match 2.2%; Score 78.8; DB 13; Length 589;
 Best Local Similarity 69.5%; Pred. No. 2.8e-07;
 Matches 107; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1307 GCCCTGGAGCCCTCCATCTCCAAAGGAGATCATGACCCCTTCAACACCAAGCACCATCAG 1366
 Db 122 GCGCTGGAGCCACACATTAACGGGCAGATCATGCGCTGCACCAAGCACCATCGG 181
 QY 1367 ACTTATGTTAAAGGCTCAAGCGTCCGAGGAGAGTACTCGGCCGCTGTGGGCAAGGAG 1426
 Db 182 GCCTACGTGAACACACCTCAACGCCACCGAGGAGAGTACCACGAGGCTCTGGCCAAGGGA 241
 QY 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
 Db 242 GATGTTACAACCTCAGGTGCTCTTCAGCCTGCAC 275

Search completed: April 1, 2004, 21:52:24
 Job time : 9345 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 10:57:14 ; Search time 255.87 Seconds
(without alignments)
7877.372 Million cell updates/sec

Title: US-09-727-855B-1

Perfect score: 3632

Sequence: 1 tctgttgataatctttcta.....aagagcttgaccattgttag 3632

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94.8	2.6	7218	1	US-08-232-463-14
2	84.2	2.3	728	4	US-09-091-097-5
3	74	2.0	813	2	US-08-927-230A-1
4	74	2.0	813	3	US-09-151-052-1
5	74	2.0	829	4	US-09-023-655-1348
6	74	2.0	1032	6	5240847-25
7	72.4	2.0	594	3	US-09-075-019-1
8	72.4	2.0	581	3	US-09-075-019-6
9	72.4	2.0	569	3	US-08-365-486A-27
10	72.4	2.0	969	3	US-08-880-342-27
11	72.4	2.0	976	3	US-09-126-109-1
12	72.4	2.0	3789	3	US-09-075-019-8
13	71	2.0	3300	2	US-08-928-692-29
14	71	2.0	3300	4	US-09-339-972-29
15	70.8	1.9	977	2	US-08-023-980B-2
16	70.8	1.9	977	4	US-09-091-097-7
17	66.2	1.8	812	4	US-08-486-953A-2
18	65.2	1.8	1143	4	US-09-373-731-1
19	64.4	1.8	600	6	5240847-16
20	63.6	1.8	630	4	US-09-091-097-29
21	62.8	1.7	600	6	5240847-9
22	62.8	1.7	600	6	5240847-17
23	62.8	1.7	987	6	5240847-19
24	62.4	1.7	535	6	5240847-6
25	62.4	1.7	623	6	5240847-1
26	61.2	1.7	600	6	5240847-8
27	60	1.7	7218	1	US-08-232-463-14

c 27

Sequence 41, Appl
Sequence 42, Appl
Sequence 23, Appl
Patent No. 5240847
Sequence 34, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 33, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 37, Appl
Sequence 43, Appl
Sequence 8022, Ap
Sequence 7972, Ap
Sequence 8294, Ap
Sequence 13, Appl
Sequence 41, Appl
Sequence 40, Appl

58 1.6 495 1 US-08-133-711-41
57.6 1.6 491 1 US-08-133-711-42
56.8 1.6 621 4 US-09-214-909-23
55.8 1.5 522 6 5240847-5
52.8 1.5 491 1 US-08-133-711-34
51.2 1.4 491 1 US-08-133-711-38
51.2 1.4 491 1 US-08-133-711-39
50.6 1.4 491 1 US-08-133-711-33
49.8 1.4 4403765 3 US-09-103-840A-2
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49.6 1.4 491 1 US-08-133-711-37
49 1.3 490 1 US-08-133-711-43
48.8 1.3 624 4 US-09-252-991A-8022
48.8 1.3 705 4 US-09-252-991A-7972
48.8 1.3 999 4 US-09-252-991A-8294
47.6 1.3 306 4 US-09-091-097-13
47.6 1.3 427 4 US-09-091-097-41
47.4 1.3 491 1 US-08-133-711-40

ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptz9pt-f1s
; US-08-232-463-14

Query Match 2.6%; Score 94.8; DB 1; Length 7218;

NAME/KEY: mat_peptide
LOCATION: 115..708
US-08-927-230A-1

Query Match 2.0%; Score 74; DB 2; Length 813;
Best Local Similarity 67.5%; Pred. No. 2e-12;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Db 271 GATGTTACAGCCAGATAGCTCTTACGCTGCAC 304

RESULT 4

US-09-151-052-1
Sequence 1, Application US/09151052
Patent No. 6107070
GENERAL INFORMATION:
APPLICANT: Nick et al.
TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Floor 24
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,052
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/927,230
FILING DATE: September 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: UFG-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 43..708
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 115..708
US-09-151-052-1

Query Match 2.0%; Score 74; DB 3; Length 813;
Best Local Similarity 67.5%; Pred. No. 2e-12;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCCTTCAACACCAAGCACCATCAG 1366
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QY 1367 ACTTATGTTAAAGCCCTCAACGCTGCCGAGGAGAGTACTCGGCCGCTGTGGCAAGGAG 1426
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Db 211 GCCTAGCTGAACAACCTGAACGTCACCGAGGAGAGTACCGAGGAGGCTTGGCCAGGGA 270
QY 1427 GATGTGCTTACCAGGTTAAGCTTCACTCTGTAC 1460
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Db 271 GATGTTACAGCCAGATAGCTCTTACGCTGCAC 304

RESULT 5

US-09-023-655-1348
Sequence 1348, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1348:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g34710
US-09-023-655-1348

Query Match 2.0%; Score 74; DB 4; Length 829;
Best Local Similarity 67.5%; Pred. No. 2e-12;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCCTTCAACACCAAGCACCATCAG 1366
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Db 175 GCCTGGAACTCATCATCAACGGCGAGATCATGAGCTGCACCAAGCACCACGCG 234
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Db 235 GCCTAGTGAACACCTGAAGCTCACCGAGGAGAGTACCGAGGCGGTGGCCAAAGGA 294
QY 1427 GATGTGTTACCGAGGTTAAGCTTCACTGCTGTAC 1460
Db 295 GATGTACGCCAGATAGCTCTTCAGCCTGCAC 328

RESULT 6
5240847-25
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ERLINBORG;
; ZOPHEL, ANDREAS; KRYSTEK, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HWN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO:25:
; LENGTH: 1032
5240847-25

Query Match 2.0%; Score 74; DB 6; Length 1032;
Best Local Similarity 67.5%; Pred. No. 2.4e-12;
Matches 104; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCCTTACCACCAAGCACCATCAG 1366
Db 109 GCCCTGGAACCTCATACACGCGGAGATCATGAGCTGCGACCAAGCACCACGCG 168
QY 1367 ACTTATGTTAAGCGCCTCAAGCTGCCGAGGAGTACTCGGCGGTGTGGCAAGGAG 1426
Db 169 GCCTACGTGAACACCTGAAGCTACCGAGGAGAGTACCGAGGCGGTGGCCAAAGGA 228
QY 1427 GATGTGTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
Db 229 GATGTACGCCAGATAGCTCTTCAGCCTGCAC 262

RESULT 7
US-09-075-019-1
; Sequence 1, Application US/09075019
; Patent No. 6190658
; GENERAL INFORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..681
; US-09-075-019-6

Query Match 2.0%; Score 72.4; DB 3; Length 681;
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 594 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..594
US-09-075-019-1

Query Match 2.0%; Score 72.4; DB 3; Length 594;
Best Local Similarity 66.9%; Pred. No. 4.9e-12;
Matches 103; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCCATCTCCAAGGAGATCATGACCCCTTACCACCAAGCACCATCAG 1366
Db 37 GCCCTGGAACCTCATACACGCGGAGATCATGAGCTGCGACCAAGCACCACGCG 96
QY 1367 ACTTATGTTAAGCGCCTCAAGCTGCCGAGGAGTACTCGGCGGTGTGGCAAGGAG 1426
Db 97 GCCTACGTGAACACCTGAAGCTCACCGAGGAGAGTACCGAGGCGGTGGCCAAAGGA 156
QY 1427 GATGTGTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
Db 157 GATGTACGCCAGATAGCTCTTCAGCCTGCAC 190

RESULT 8
US-09-075-019-6
; Sequence 6, Application US/09075019
; Patent No. 6190658
; GENERAL INFORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..681
; US-09-075-019-6

Query Match 2.0%; Score 72.4; DB 3; Length 681;
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Best Local Similarity		66.9%;	Pred. No. 5.5e-12;	
Matches	103;	Conservative	0;	Mismatches 51;
			Indels	0;
			Gaps	0;
Qy	1307	GCCCTGAGCCCTCATCTTCAAGGAGTATGACCCCTTACACACCAAGCACCATCAG	1366	
Db	43	GCCCTGAACCTCATCAACGCGCATCATGAGCTGCACACAGCACCACGCG	102	
Qy	1367	ACTTATGTTAAGCGCCCTCAACGCTGCCGAGGAGAGCTACTCGGCCGTGTGGGCAAGGAG	1426	
Db	103	GCCTACGTGACAACTGAACGTCACCGAGGAGAAGTACCAGGAGGCGTTGGCCCAAGGA	162	
Qy	1427	GATGTGTTACCCAGGTTAAGCTTCAGTCTGTAC	1460	
Db	163	GATGTTACGCCAGACAGAGCTCTTTCAGCCTGCAC	196	

RESULT 9
 US-08-365-486A-27
 ; Sequence 27, Application US/08365486A
 ; Patent No. 5834306
 ; GENERAL INFORMATION:
 ; APPLICANT: Webster, Keith A.
 ; APPLICANT: Bishopric, Nanette H.
 ; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 ; TITLE OF INVENTION: Therapeutic Constructs
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Denlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/365,486A
 ; FILING DATE: 23-DEC-1994
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sholtz, Charles K.
 ; REGISTRATION NUMBER: 38,615
 ; REFERENCE/DOCKET NUMBER: 8255-0018
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 969 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: human manganese superoxide dismutase
 ; INDIVIDUAL ISOLATE: EMBL #X59445
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 61..729
 ; US-08-365-486A-27

	Query Match	2.0%	Score 72.4	DB 2	Length 969
	Best Local Similarity	66.9%	Pred. No. 7.2e-12		
	Matches 103	Conservative	0	Mismatches 51	Indels 0
				Gaps 0	
QY	1307	GCCTGGAGCCTCCATCTCCAAAGGAGATCATGACCCCTTCACACACCAAGCACCATCAG	1366		
Db	169	GCCTTGGAACTTCATCATCAACGCGGAGATCATGCAGTGTGACACAGCAAGCACCAACGCG	228		

Qy	1367	ACTATGTTAACGGCTCAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGCAAGGAG	1426
Db	229	GCCTACTGTGAACAACTTGACCTCAACGAGGAGAAGTACAGAGGCGTTTGGCCAAAGGGA	288
Qy	1427	GATGTGTTACCCAGGTTAAGCTTCAGTCTGTAC	1460
Db	289	GATGTTACAGCCAGATAGCTTTTCAGCCTGCAC	322

RESULT 10
US-08-880-342-27
; Sequence 27, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 969 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: human manganese superoxide dismutase
; INDIVIDUAL ISOLATE: EMBL #X59445
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..729
US-08-880-342-27

Query Match 2.0%; Score 72.4; DB 3; Length 969;
Best Local Similarity 66.9%; Pred. No. 7.2e-12;
Matches 103; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1307 GCCTGGAGCCCTCATCTCCAAAGGAGATCATGACCTTACACCAAGCACCATCAG 1366
Db 169 GCCCTGGAACCTCATCAACGCCGAGATCATGAGCTGACACAGCAACCAACGCG 228
QY 1367 ACTTATGTAAAGCGCTCAACGCTGCCGAGGAGAGTACTCGCGCTGTGGGCAAGGAG 1426
Db 229 GCCTACGTGAACACCTGACGTCACAGGAGAAGTACCAAGGAGGCGTTGGCCAAGGGA 288
QY 1427 GATGTGTTACCCAGGTTAAAGCTTCAGTCTGTAC 1460
Db 289 GATGTTACAGCCACGATAGCTCTTACAGCCTGCAC 322

RESULT 11
US-09-126-109-1
; Sequence 1, Application US/09126109
; Patent No. 6171856
; GENERAL INFORMATION:
; APPLICANT: Thigpen, Anice
; APPLICANT: Hohmeier, Hans-Ewald
; APPLICANT: Newgard, Christopher B.
; APPLICANT: Unger, Roger H.
; APPLICANT: Shimabukuro, Michio
; APPLICANT: Chen, Guaxun
; APPLICANT: Rhodes, Christopher J.
; APPLICANT: Hugl, Sigrun R.
; APPLICANT: Cousin, Sharon
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
; TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/126,109
; FILING DATE: 30-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/055,092
; FILING DATE: 30-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US Unknown
; FILING DATE: 03-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabeela R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: UTSD:560
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 976 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-126-109-1

Query Match 2.0%; Score 72.4; DB 3; Length 976;
Best Local Similarity 66.9%; Pred. No. 7.2e-12;
Matches 103; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 1307 GCCTGGAGCCCTCATCTCCAAAGGAGATCATGACCTTACACCAAGCACCATCAG 1366

Db 203 GCCCTGGAACCTCATCAACGCCGAGATCATGAGCTGACACAGCAACCAACGCG 262
QY 1367 ACTTATGTAAAGCGCTCAACGCTGCCGAGGAGAGTACTCGCGCTGTGGGCAAGGAG 1426
Db 263 GCCTACGTGAACACCTGACGTCACCGAGGAGAGTACCAAGGAGGCGTTGGCCAAGGGA 322
QY 1427 GATGTGTTACCCAGGTTAAAGCTTCAGTCTGTAC 1460
Db 323 GATGTTACAGCCACGATAGCTCTTACAGCCTGCAC 356

RESULT 12
US-09-075-019-8
; Sequence 8, Application US/09075019
; Patent No. 6190658
; GENERAL INFORMATION:
; APPLICANT: UTC IR459
; TITLE OF INVENTION: A GENETICALLY MODIFIED MANGANESE
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE FOR TREATING OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,019
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2848-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-075-019-8

Query Match 2.0%; Score 72.4; DB 3; Length 3789;
Best Local Similarity 66.9%; Pred. No. 2e-11;
Matches 103; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 1307 GCCTGGAGCCCTCATCTCCAAAGGAGATCATGACCTTACACCAAGCACCATCAG 1366
Db 586 GCCCTGGAACCTCATCAACGCCGAGATCATGAGCTGACACAGCAACCAACGCG 645
QY 1367 ACTTATGTAAAGCGCTCAACGCTGCCGAGGAGAGTACTCGCGCTGTGGGCAAGGAG 1426
Db 646 GCCTACGTGAACAACTGAACTGACCGAGGAGAAGTACCAAGGAGGCGTTGGCCAAGGGA 705
QY 1427 GATGTGTTACCCAGGTTAAAGCTTCAGTCTGTAC 1460
Db 706 GATGTTACAGCCACGATAGCTCTTACAGCCTGCAC 739

RESULT 13
US-08-928-692-29
; Sequence 29, Application US/08928692

```

; Patent No. 5958727
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5958727o No. 5958727disk of No. 5958727th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,692
; FILING DATE: 12-SEPT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-928-692-29

Query Match          2.0%; Score 71; DB 2; Length 3300;
Best Local Similarity 62.9%; Pred.No.5e-11;
Matches 110; Conservative 0; Mismatches 65; Indels 0; Gaps 0

QY      1281 TTGGTTGAAAATTCTCTCCACTCAGGCCCTGGAGGCCTTCATCTCCAAGGAGATCATGA 134
           |||||
Db       852 TTGACGTGAATACAGATCACTATGGCGCCCTTGAGCCCTCTAUTC CGGAAAGATCATGG 911

QY      1341 CCCTTCAACACCAAGCACCATCAGACTTATGTTAAAGCGCTCAACGTCGCGAGGAGA 140
           |||||
Db       912 AGCTTCAACCACAAGAACCAACCACCAGACCTATGTCACACAGCTACACACGCCCATCGAAC 971

QY      1401 GCTACTCGGCGCTGTGGCGAAGGAGATGTCTTACCCAGGTTAGCTTCAGTC 1455
           |||||
Db       972 AGCTCCAGGAGGCGCTGCGCAAGGAGGACATCACCACCTCAGATCAACCTCAAGCC 1026


RESULT 14
US-09-339-972-29
; Sequence 29, Application US/09339972
; Patent No. 6323002
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Yaver, Deborah S.
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6323002o No. 6323002disk of No. 6323002th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
```

```

STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,972
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,692
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944,200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 3300 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-339-972-29

Query Match 2.0%; Score 71; DB 4; Length 3300;
Best Local Similarity 62.9%; Pred. No. 5e-11;
Matches 110; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1281 TTGTTGAAATTCCTCTCCACTCAGCCCTCGAGCCCTCCATCTCCAAAGAGATCATGA 1340
Db 852 TTGACTGAATTAACAGATGACTATGGGCCCTTGAGCCCTCTATCTCCGGAAGATCATGG 911
QY 1341 CCTTCACACACCAAGCACCATCAGACTTATGTAAACGGCCTCAACGCTGCCGAGGAGA 1400
Db 912 AGTTTCACCAAGACCACACGACCTATGTCAACAGCTATCAACACCGCCATCGAAC 971
QY 1401 GCTACTGGCGCTGTGGCAAGGAGATGTGTTACCCAGGTTAAGCTTTCAGTC 1455
Db 972 AGCTCAGGAGGCGTCGCCAAGGAGACATCACCACCTCAGATCAACCTCAAGCC 1026

RESULT 15
US-08-023-980B-2
Sequence 2, Application US/08023980B
Patent No. 5843641
GENERAL INFORMATION:
APPLICANT: Brown, Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 585 Commercial Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-1024
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/023,980B
FILING DATE: 26-FEB-1993

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/177001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/723-4123
; TELEFAX: 617/723-8962
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-023-980B-2

Query Match      1.9%; Score 70.8; DB 2; Length 977;
Best Local Similarity 66.2%; Pred. No. 2.3e-11;
Matches 102; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1307 GCCCTGGAGCCCTCCATCTCCAAAGAGATCATGACCCCTTACCAACCAAGCACCATCAG 1366
Db 204 GCCCTGGAACTTCATCAATCAACGCGCAGATCATGCGAGCTGCACACAGCAAGCACCACGCG 263

QY 1367 ACTTATGTTAAGCGCTCAACGCTGCCGAGGAGAGTACTCGCGCGCTGTGGGCAAGGAG 1426
Db 264 GCCTACGTGAACAACCTGAACCTACCGAGGAGAGTACCAAGAGGCGGTGGCAAGGGA 323

QY 1427 GATGTGCTTACCCAGGTTAAGCTTCAGTCTGTAC 1460
Db 324 GATGTTACAGCCACACACGCTCTTCAGCCTGCAC 357

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Search completed: April 1, 2004, 13:45:30
Job time : 266.87 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 10:57:14 ; Search time 47.1302 Seconds
(without alignments)
7877.372 Million cell updates/sec

Title: US-09-727-855B-4
Perfect score: 669
Sequence: 1 atgtctgttcgagcatccct.....gattgcaggctgtctctaa 669

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	252	37.7	728	4	US-09-091-097-5
2	250.6	37.5	812	4	US-09-091-097-7
3	220.6	33.0	630	4	US-09-091-097-29
4	199.4	29.8	813	2	US-08-927-230A-1
5	199.4	29.8	813	3	US-09-151-052-1
6	199.4	29.8	829	4	US-09-023-655-1348
7	197.8	29.6	1032	6	5240847-25
8	196.2	29.3	969	2	US-08-365-486A-27
9	196.2	29.3	969	3	US-08-880-342-27
10	196.2	29.3	976	3	US-09-126-109-1
11	194.6	29.1	977	2	US-08-023-980B-2
12	194.6	29.1	977	2	US-08-486-953A-2
13	194.4	29.1	3789	3	US-09-075-019-8
14	194	29.0	594	3	US-09-075-019-1
15	194	29.0	681	3	US-09-075-019-6
16	184.4	27.6	600	6	5240847-16
17	182.8	27.3	600	6	5240847-9
18	182.8	27.3	600	6	5240847-17
19	182.8	27.3	987	6	5240847-19
20	181.2	27.1	600	6	5240847-8
21	165.6	24.8	535	6	5240847-6
22	165.6	24.8	623	6	5240847-1
23	157.4	23.5	522	6	5240847-5
24	155.8	23.3	3300	2	US-08-928-692-29
25	155.8	23.3	3300	4	US-09-339-972-29
26	154	23.0	621	4	US-09-214-909-23
27	142	21.2	371	4	US-09-091-097-25

28 139.2 20.8 4403765 3 US-09-103-840A-2 Sequence 2, Appli
29 139.2 20.8 4411529 3 US-09-103-840A-1 Sequence 1, Appli
30 139 20.8 1143 4 US-09-373-731-1 Sequence 1, Appli
31 134.6 20.1 1230025 4 US-09-198-452A-1 Sequence 1, Appli
32 123.8 18.5 491 1 US-08-133-711-44 Sequence 44, Appli
33 121.8 18.2 654 4 US-09-489-039A-5056 Sequence 5056, Ap
34 121.8 18.2 702 4 US-09-489-039A-4999 Sequence 4999, Ap
35 121.6 18.2 491 1 US-08-133-711-40 Sequence 40, Appli
36 119.6 17.9 624 4 US-09-252-991A-8022 Sequence 822, Ap
37 119.6 17.9 999 4 US-09-252-991A-8022 Sequence 822, Ap
38 117.4 17.5 491 1 US-08-133-711-36 Sequence 36, Appli
39 115.8 17.3 491 1 US-08-133-711-37 Sequence 37, Appli
40 114.2 17.1 491 1 US-08-133-711-34 Sequence 34, Appli
41 112 16.7 491 1 US-08-133-711-32 Sequence 32, Appli
42 111.4 16.6 721 4 US-09-262-856A-8 Sequence 8, Appli
43 111 16.6 491 1 US-08-133-711-38 Sequence 38, Appli
44 111 16.6 491 1 US-08-133-711-39 Sequence 39, Appli
45 110.4 16.5 491 1 US-08-133-711-33 Sequence 33, Appli

ALIGNMENTS

RESULT 1
US-09-091-097-5
; Sequence 5, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; TITLE OF INVENTION: MALASSEZIA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 728 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..618

US-09-091-097-5

Query Match 37.7%; Score 252; DB 4; Length 728;
Best Local Similarity 65.5%; Pred. No. 5e-68;
Matches 385; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 68 TCAGGGAAGATACCTGCTGAGTCTTCTTACGCTTACGATGCGCTGAGCCCTCCCA 127
DB 8 TCATGACTGATGACACTCTCCCTCTCTGCGCTTACGCTTACGATGCGCTGAGCGGCTTTA 67

QY 128 TCTCAAGGAGATCATGACCCCTTCAACACACCAAGCACCACATGACTTATGTTAACGCC 187
DB 68 TCCTTAAGGAGATCATGACGCTTCAACACACCAAGCACCACATGACTTATGTTAACGCC 127

QY 188 TCAACGCTGCGAGGAGAGTACTGCGCGCTGTGGGCAAGGAGATGTGTTTACCAGG 247
DB 128 TCAACGCGCGCGAAGAGGCTGACGTGAGGCGCGCGCAAGGAGCTGTTTAAAGCAGA 187

QY 248 TTAAGCTTCACTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTCT 307
DB 188 TCCAGCTGACAGTGGGATCAAGTTCAACGCGGTGGCCACATCAACCACTCGCTGTCT 247

QY 308 GGAAGAACTTGGCTCCCTATGATCCGAGGAGGCTTACCTCTCTCAAGGACCTCTCAAGA 367
DB 248 GGAAGAACTTGGCTCCCTATGATCCGAGGAGGCTTACCTCTCTCAAGGACCTCTCAAGC 307

QY 368 AGGCTATCGAGGAATCTTTTGGTCTTTCGAGGCGCTTCAAGAGAGTTCAACGCTGACA 427
DB 308 AGGCATCGAGCAGGAGTTCGGCGACTTTGAGAAGTTCAAGCAGCACCCTTCAACAGGAGG 367

QY 428 CGCTGTGTTCCAGGATCCGATCGGCTGGCTGGCTTGAACCCGCTTACTAAGAAAGC 487
DB 368 CGCGCGGATCCAGGTTTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 424

QY 488 TGAAGTCAACACGACCGCAACAGGAGGCTTCTGCTTACTTACTTACTTACTTACTTACT 547
DB 425 TCGACTGCTGTTGCCAAGGACGAGGAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGG 484

QY 548 TTGACATCTGGAGCAGCTTCTTACCTTCACTTCACTTCACTTCACTTCACTTCACTTCA 607
DB 485 GGGATGGCTGGGAGCAGCTTCTTACCTTCACTTCACTTCACTTCACTTCACTTCACTTCA 544

QY 608 CTGCTGTTGGTTCGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 655
DB 545 AGGCTGTTGGTTCGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 592

RESULT 2

US-09-091-097-7

Sequence 7, Application US/09091097
Patent No. 6432407

GENERAL INFORMATION:

APPLICANT: TAKESAKO, KAZUHO
APPLICANT: OKADO, TAKASHI
APPLICANT: YAGIHARA, TOMOKO
APPLICANT: KURODA, MASANOBU
APPLICANT: ONISHI, YOSHIMI
APPLICANT: KATO, IKUNOSHIN
APPLICANT: AKIYAMA, KAZUO
APPLICANT: YASUEDA, HIROSHI
APPLICANT: YAMAGUCHI, HIDEYO

TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
TITLE OF INVENTION: MALASSEZIA
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0346P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..673
US-09-091-097-7

Query Match 37.5%; Score 250.6; DB 4; Length 812;
Best Local Similarity 63.9%; Pred. No. 1.4e-67;
Matches 379; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

QY 74 CAAAGATACCTGCTGAGTCTTCTTACGCTTACGATGCGCTGAGGAGGCTTCACTTCA 133
DB 72 CCAAGTACACGCTGCGCGCTGCGTACGACTAGCGCGCTGAGCGGCGATCTCGG 131

QY 134 AGGAGATCATGACCTTCCACACCAAGCACCACATGACTTATGTTTAAAGGCTTCAAGC 193
DB 132 GCGAGATCATGAGAGCAGCTACGAGAGAGCACCACCGACCTACGTCACACCTGAAGC 191

QY 194 CTGCGGAGGAGAGTACTCTGCGCGCTGTGGGCAAGGAGGATGTGTTTACCCAGGTTAAGC 253
DB 192 CGCGGAGGAGAGTGTGATCGACGCGCTCCCGCAGCAGAGCGCTCGCGAGATTGCGC 251

QY 254 TTCACTGCTCTCAAGTTTCAACGAGGAGGAGCAGATCAATCACTCTCTGTTTCTGAGA 313
DB 252 AGCTGAACGCGATCAAGTTCAACGCGGTGGCCACATCAACCACTCGCTCTTCTGAGA 311

QY 314 ACTTGGCTCCCTATGATCCGAGGAGGCTACCTCTCTGAAGGAGCTCTCAAGAGGCTA 373
DB 312 ACCTCGCGCGAGCAAGAGGCGCGGAGCTGACTCGGCGAGCTGCGCTCGCGA 371

QY 374 TCGAGGAATCTTTTGGTCTTTTCGAGGCGCTTCAAGAGAGTTCACCGTGAACGCTG 433
DB 372 TCGACGCGGACTTTGGCTCGGCTCGACGCGCATGAAGAGAGTTCACCGCGGCTCGCG 431

QY 434 CTGTCCAAGGATCCGAGTGGGCTGGCTTGGCTTGAACCGCTTACTAGAGAGCTGGAAG 493
DB 432 GCATCCAGGCGAGCGCTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 491

QY 494 TCACCAAGCAGCGCCACACGAGGAGGCTTCTGCTTACTTCACTTCTATCATCGGAGTTGACA 553
DB 492 TCATACAGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 551

QY 554 TCTGGGAGCAGCGCTTCTTACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 613
DB 552 CGTGGGAGCAGCGGTTTCTTACCTTCACTTCACTTCACTTCACTTCACTTCACTTCA 611

QY 614 TTGAGTCCGTTATCAACTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 666
DB 612 TCTGAGCAGGATCAACTTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 664

RESULT 3

US-09-091-097-29

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; Sequence 29, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; TITLE OF INVENTION: MALASSEZIA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 630 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; US-09-091-097-29

Query Match 33.0%; Score 220.6; DB 4; Length 630;
Best Local Similarity 52.5%; Pred. No. 2.3e-58;
Matches 343; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

QY 118 GAGCCCTCCATCTCCAAGGAGATCATGACCCCTTCCACACAGGAGGAGGAGGATG 177
Db 1 GAACCTGCTTTCGGGGGAGATAATGGAGACGCACTACGAGAAGGAGGAGGAGGAGG 60

QY 178 GTTAAGGGCTCAACGCTGCGGAGGAGAGCTACTCGCGCGCTGTGGGCAAGGAGGATG 237
Db 61 GTCAACAACCTGAACCGCGGAGGAGCAAGCTGATGACGCGCTCCGCGAGGAGCCCG 120

QY 238 CTTACCCAGGTTAAGTTTCACTGTCTCTCAAGTTCAACGGAGGAGGAGGAGGAGGAGG 297
Db 121 CTCGGGAGATTGCGCAGCTGAACGCGATCAANTTCATCGGCGGTGGCCACATCAACCAC 180

QY 298 TCTCTCTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 357
Db 181 TGCTCTCTTCTGGAAGAACCTTCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240

QY 358 CCTCTCAAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 417
Db 241 GAGCTGGCTCCGCGATGACCGCGAGTTTGGCTCGGTGCGACCCGAGGAGGAGGAGGAG 300

QY 418 AAGCTGTACACCGCTCTGTCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 477
Db 118 AAGCTGTACACCGCTCTGTCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 477

; Sequence 30, Application US/08927230A
; Patent No. 5985633
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,230A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: UFJ-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..708
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 115..708
; US-08-927-230A-1

Query Match 29.8%; Score 199.4; DB 2; Length 813;
Best Local Similarity 61.1%; Pred. No. 9.2e-52;
Matches 367; Conservative 0; Mismatches 216; Indels 18; Gaps 2;

QY 301 AACGCGGCTCGCGGCATCCAGGATATCGGCTGGGCTGGCTCGGCTGAACCCACG 360
QY 478 ACTAAGAGCTGGAAGTCACACGACCGCAACAGGACCCCTCTGCTTACTCAATTCCT 537
Db 361 ACGCAGAAGCTCGACATCATCAGACCGCAACAGGACCCGCTCTCTGTGCAAGCG 420
QY 538 ATCATCGAGTTGACATCTGGGACGCTTCTTACCTTCACTACAGAGGAGGAGGAGG 597
Db 421 CTGATTGGCATCGATGCTGGGAGCAGCGTACTTACCTGAGTACAAGAGGAGGAGG 480
QY 598 GACTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
Db 481 GACTACTTCAAGCGATCTGACCGTGTCACTTTGAGGAGGCGGAGAGCGTCTCANG 540
QY 658 GCTGCTCTC 666
Db 541 GAGGCGCTC 549

RESULT 4
US-08-927-230A-1
; Sequence 1, Application US/08927230A
; Patent No. 5985633
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,230A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: UFJ-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..708
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 115..708
; US-08-927-230A-1

Query Match 29.8%; Score 199.4; DB 2; Length 813;
Best Local Similarity 61.1%; Pred. No. 9.2e-52;
Matches 367; Conservative 0; Mismatches 216; Indels 18; Gaps 2;

QY 69 CAGGCAAGCATACCTCGCTGAGTCTCTTACGCTTACGATGCCCTGAGGAGGAGGAGG 128
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GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1348:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G34710
US-09-023-655-1348

Query Match          29.8%; Score 199.4; DB 4; Length 829;
Best Local Similarity 61.1%; Pred. No. 9.2e-52;
Matches 367; Conservative 0; Mismatches 216; Indels 18; Gaps 2;

QY 69 CAGGCGAAAGCATACCCCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
Db 132 CAGGCGAAAGCATACCCCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 191

QY 129 CTCGAAGGAGATCATGACCCCTTCCACACCAAGACACCATCAGACTATGTTTAAAGCCCT 188
Db 192 CAACGCGCAGATCATGACGCTGACACCAAGACACCATCAGCGCCCTACGTGAACACCT 251

QY 189 CAACGCTGCCGAGGAGAGTACTCGCCGCTGCGGAGGAGGAGGAGTGTCTTACCCAGGT 248
Db 252 GAACGTCAACGAGGAGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 311

QY 249 TAAGCTTTCAGTCTCTCAAGTTCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 308
Db 312 AGCTCTTCAGCTGCACTGAAGTTCAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 371

QY 309 GAAGAACTTGGCTCCCTATGAGATCCGAGGAGGAGTACCCTCTCTGAAGGAGGAGGAGGAGGAG 368
Db 372 GACAAACCTTCAGCCCTTAAACGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 422

QY 369 GCGTATCGAGGAGTCTTTTGGTCTTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 428
Db 423 AGCCATCAAAACGAGTCTTTGGTCTTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 482

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QY 429 CGCTGCTGTCCAAAGGATCCGCGATGGGGCTG3CTTGGCTTGAACCCGCTTACTAAGAAGCT 488
Db 483 TGTGTGTGTCCAAAGGCTCAGGTTGGGTTGGCTTGGTTTCAATAAGCAACGGGACACTT 542

QY 489 GGAAGTCACACGACCGCCCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 539
Db 543 ACAAAATTGCTGCTTGTCTCAAAATCAGGATCCACTGCAAGGAGGAGGAGGAGGAGGAGGAGGAG 602

QY 540 CATCGGAGTTGACATCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 599
Db 603 GCTGGGAGTTGATGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 662

QY 600 CTATCTCGCTGCTGTTTGGTTCCTTCAACTACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 659
Db 663 TTAATCTAAAGCTATTGTAATCAACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 722

QY 660 T 660
Db 723 T 723

RESULT 7
5240847-25
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSTEK, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO: 25;
; LENGTH: 1032
5240847-25

Query Match          29.6%; Score 197.8; DB 6; Length 1032;
Best Local Similarity 60.9%; Pred. No. 3.2e-51;
Matches 366; Conservative 0; Mismatches 217; Indels 18; Gaps 2;

QY 69 CAGGCGAAAGCATACCCCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
Db 66 CAGGCGAAAGCATACCCCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 125

QY 129 CTCGAAGGAGATCATGACCCCTTCCACACCAAGACACCATCAGACTATGTTTAAAGCCCT 188
Db 126 CAACGCGCAGATCATGACGCTGCACCAAGACACCATCAGCGCCCTACGTGAACACCT 185

QY 189 CAACGCTGCCGAGGAGAGTACTCGCCGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 248
Db 186 GAACGTCAACGAGGAGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 245

QY 249 TAAGCTTTCAGTCTCTCAAGTTCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 308
Db 246 AGCTCTTCAGCTGCACTGAAGTTCAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 305

QY 309 GAAGAACTTGGCTCCCTATGAGATCCGAGGAGGAGTACCCTCTCTGAAGGAGGAGGAGGAGGAG 368
Db 306 GACAAACCTTCAGCCCTTAAACGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 356

QY 369 GCGTATCGAGGAGTCTTTTGGTCTTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 428
Db 357 AGCCATCAAAACGAGTCTTTGGTCTTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 416

QY 429 CGCTGCTGTCCAAAGGATCCGCGATGGGGCTGCTTGGCTTGAACCCGCTTACTAAGAAGCT 488
Db 417 TGTGTGTGTCCAAAGGCTCAGGTTGGGTTGGCTTGGTTTCAATAAGAAACGGGACACTT 476

QY 489 GGAAGTCACACGACCGCCCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 539
Db 477 ACAAAATTGCTGCTTGTCTCAAAATCAGGATCCACTGCAAGGAGGAGGAGGAGGAGGAGGAGGAG 536

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Db 340 AGCTCTTCAGCGCTGACCTGAAGTTCAATGGTGGTGCATATCAATCATAGCATTTTCTG 399
Qy 309 GAAGAACTTGGCTCCCTATGATCCGAGGAGGCTACCTCTCTGAGGACCTCTCAAGAA 368
Db 400 GACAAACCTCAGCCCTAAACGGTGGTGGGAGAACCCCA-----AAGGGGAGTTGCTGGA 450
Qy 369 GCCTATCAGGAATCTTTTGGTTCCTTCGAGGCTTCAAGAGAAAGTTCAACGCTGACAC 428
Db 451 AGCCATCAACCGTGACTTTGGTCTTTCGACAAAGTTTAAGGAGAGCTCAGCGCTGCATC 510
Qy 429 CGCTGCTGTCCAAAGATCCGATGGGCTGGCTTGGCTTGAACCGCTTACTPAAGAGCT 488
Db 511 TGTGGTGTCCAAGGCTCAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 570
Qy 489 GGAAGTACCAGCAGCGCCCAACGAGACCTCTGCTTACT-----CACATTCCTAT 539
Db 571 ACAAAATGCTGCTTGTCCAAATCAGGATCCACTGCAAGAAACACAGGCTTTATTCCTACT 630
Qy 540 CATCGAGTTGACATCTGGGAGCAGCTTCTTACCTTCAGTACAAGAACGTCAGGCTTGA 599
Db 631 GCTGGGATGATGTGGGAGCAGCTTACTTACCTTCAGTATAAAATGTACAGGCTTGA 690
Qy 600 CTATCTCGCTGCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 659
Db 691 TTATCTAAAGCTAATTTGGAATGTAATCAACTGGGAGAGTGAATCACTGAAAGATACATGCG 750
Qy 660 T 660
Db 751 T 751

RESULT 11

US-08-023-980B-2
; Sequence 2, Application US/08023980B
; Patent No. 5843641
; GENERAL INFORMATION:
; APPLICANT: Brown, Robert
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Rosen, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
; TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 585 Commercial Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-1024
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/023,980B
; FILING DATE: 26-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/177001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/723-4123
; TELEFAX: 617/723-8962
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA
US-08-023-980B-2

Query Match 29.1%; Score 194.6; DB 2; Length 977;
Best Local Similarity 60.6%; Pred. No. 3e-50;
Matches 364; Conservative 0; Mismatches 219; Indels 18; Gaps 2;

Qy 69 CAGGCAAGCATACCTTCGCTGAGCTTCCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
Db 161 CAGGCAAGCAGACAGCTCCCGACCTCCCTACGACTACGGCGCCCTGGAACTCAT 220
Qy 129 CTCGAAGAGATCATGACCTTCCACCAAGCAAGCACCATCAGACTTATGTTAAAGGCT 188
Db 221 CAACGCGCAGATCATGACAGCTGCACCAAGCAAGCACCACGCGGCTACGTGAACACCT 280
Qy 189 CAACGCTCCGAGGAGAGCTACTCGCGCTGTGGCAAGGAGGATGCTTACCCAGT 248
Db 281 GAACCTCAGGAGGAGAGTACGAGGCGGTGGCAAGGAGAGTGTACAGCCAGAC 340
Qy 249 TAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTTCTG 308
Db 341 AGCTCTTCAGCTGACCTGAGTTCAATGGTGGTGTCTATATCAATCATAGCATTTCTG 400
Qy 309 GAAGAACTTGGCTCCCTATGATCCGAGGAGGCTACCTCTCTGAGGACCTCTCAAGAA 368
Db 401 GACAAACCTCAGCCCTAAACGGTGGTGGAGAACCCCA-----AAGGGGAGTTGCTGGA 451
Qy 369 GCCTATCAGGAATCTTTTGGTCTTTCGAGGCTTCAAGAGAGAGTTCAACGCTGACAC 428
Db 452 AGCCATCAACGAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 511
Qy 429 CGCTGCTGTCCAAGGATCCGATGGGCTGGCTTGGCTTGAACCGCTTACTTAAGAAGCT 488
Db 512 TGTGGTGTCCAAGGCTCAGGTGGGTTGGCTGGTTTCAATAAGGAGCGGACACTT 571
Qy 489 GGAAGTACCAGCAGCGCCCAACGAGGACCTCTGCTTACT-----CACATTCCTAT 539
Db 572 ACAAAATGCTGCTTGTCCAAATCAGGATCCACTGCAAGGAAACACAGGCTTTATTCCTACT 631
Qy 540 CATCGAGTTGACATCTGGGAGCAGCTTCTACCTTCAGTACAAGAACGTCAGGCTTGA 599
Db 632 GCTGGGAGTATGATGTGGGAGCAGCTTACTTACCTTCAGTATAAAATGTACAGGCTTGA 691
Qy 600 CTATCTCGCTGCTGTTGGTTCGCTTATCAACTACAAGGAGGAGGAGGAGGAGGAGGAGGAGG 659
Db 692 TTATCTAAAGCTAATTTGGAATGTAATCAACTGGGAGAGTGAATCACTGAAAGATACATGCG 751
Qy 660 T 660
Db 752 T 752

RESULT 12

US-08-486-953A-2
; Sequence 2, Application US/08486953A
; Patent No. 5849290
; GENERAL INFORMATION:
; APPLICANT: Brown, Robert
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Rosen, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
; TREATMENT AND PREVENTION OF DISEASES OF CELL DEATH
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 08:33:07 ; Search time 257.583 Seconds
(without alignments)
11033.514 Million cell updates/sec

Title: US-09-727-855B-4

Perfect score: 669

Sequence: 1 atgtctgttcagcatccct.....gattgcaggctgctctctaa 669

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	252	37.7	728	2 AAT85876	Aat85876 Malassezi
2	250.6	37.5	812	2 AAT85877	Aat85877 Malassezi
3	220.6	33.0	630	2 AAT85894	Aat85894 Malassezi
4	211.4	31.6	897	9 ADDJ5245	Add35245 Mouse mit
5	205	30.6	1492	6 ABK63720	Abk63720 Rat seque
6	205	30.6	1492	9 ADB58236	Adb58236 Toxicity-
7	203.4	30.4	1438	3 AA75734	Aaa75734 Nucleotid
8	199.4	29.8	813	1 AAN81158	Aan81158 cDNA enco
9	199.4	29.8	813	2 AAT853193	Aat853193 MnSOD cDN
10	199.4	29.8	813	2 AAT15589	Aat15589 Human man
11	199.4	29.8	813	2 AAT34277	Aat34277 Human man
12	199.4	29.8	813	2 AAX24998	Aax24998 Human nat
13	199.4	29.8	813	3 AAA63891	Aaa63891 cDNA enco
14	197.8	29.6	813	1 AAN71370	Aan71370 Sequence
15	197.8	29.6	849	6 AAN84891	Aan84891 Human man
16	197.8	29.6	849	6 ABA94453	Aba94453 Human man
17	197.8	29.6	972	7 ABX63836	Abx63836 Human cDN
18	197.8	29.6	1026	6 ABL66512	Ab166512 Lung canc
19	197.8	29.6	1026	6 ABK84524	Abk84524 Human cDN
20	197.8	29.6	1046	2 AAQ94284	Aaq94284 Human man
21	197.8	29.6	2504	4 AAL26545	Aal26545 Human bre
22	196.2	29.3	969	2 AAT31018	Aat31018 Human man
23	196.2	29.3	976	2 AAQ67474	Aaq67474 Human man

ALIGNMENTS

RESULT 1

ID AAT85876 standard; cDNA to mRNA; 728 BP.

AC AAT85876;

XX 27-AUG-2003 (revised)

DT 23-FEB-1998 (first entry)

XX Malassezia fungus MF-3 antigenic protein encoding cDNA.

XX Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;

KW allergy; antigen; ds.

OS Malassezia.

PH Key Location/Qualifiers

FT CDS 4..621

FT /*tag= a

FT /product= "MF-3_antigenic_protein"

XX WO9721817-A1.

XX 19-JUN-1997.

XX 10-DEC-1996; 96WO-JP003602.

XX 12-DEC-1995; 95JP-00346627.

PR 05-SEP-1996; 96JP-00257612.

PR 05-SEP-1996; 96JP-00257613.

XX (TAKI) TAKARA SHUZO CO LTD.

PA Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;

PI Akiyama K, Yasueda H, Yamaguchi H;

XX WPI; 1997-332788/30.

DR P-PSDB; AAW29770.

XX Antigenic proteins from the fungus Malassezia - bind to IgE antibodies

PT present in patients with Malassezia allergies, useful for diagnosis,

PT treatment and prevention of such conditions.

XX Claim 53; Page 76-77; 162pp; Japanese.

XX The present sequence encodes a specifically claimed antigenic protein

CC

Db 552 CTGGGAGACGGTTCTACCTCCAGTACAGACGTCAGGCGGACTACTTCAAGGCGA 611
 QY 614 TTTGGTCCGTTATCACTACAGAGGAGAGAGCCCGATTGAGGCTGCTCTC 666
 Db 612 TCTGGACCGTGATCACTTTGAGGAGCGGAGAGCGTCTCAAGGAGGGGCTC 664

RESULT 3
 AAT85894
 ID AAT85894 standard; cDNA to mRNA; 630 BP.
 AC AAT85894;
 XX 27-AUG-2003 (revised)
 DT 23-FEB-1998 (first entry)
 XX Malassezia fungus MF-4 antigenic protein PCR amplification fragment.
 XX Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;
 KW allergy; antigen; PCR primer; ds.
 XX Malassezia.
 OS WO9721817-Al.
 PN 19-JUN-1997.
 XX 10-DEC-1996; 96WO-JP003602.
 XX 12-DEC-1995; 95JP-00346627.
 PR 05-SEP-1996; 96JP-00257612.
 PR 05-SEP-1996; 96JP-00257613.
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
 PI Akiyama K, Yasueda H, Yamaguchi H;
 XX WPI; 1997-332788/30.
 XX Antigenic proteins from the fungus Malassezia - bind to IgE antibodies
 PT present in patients with Malassezia allergies, useful for diagnosis,
 PT treatment and prevention of such conditions.
 XX Example 14; Page 99; 162pp; Japanese.
 PS The present sequence represents a PCR amplification fragment of the MF-4
 CC antigenic protein isolated from the fungus Malassezia. The antigenic
 CC peptide can bind to IgE antibodies present in patients with allergic
 CC conditions. Antigenic proteins, peptides and nucleic acids from the
 CC fungus Malassezia can be used in the diagnosis, treatment and prevention
 CC of allergic conditions due to Malassezia organisms (such as M.furfur, M.
 CC sympodialis and M.pachydermatitis). (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX Sequence 630 BP; 156 A; 191 C; 180 G; 101 T; 0 U; 2 Other;
 SQ

Query Match 33.0%; Score 220.6; DB 2; Length 630;
 Best Local Similarity 62.5%; Pred. No. 2.1e-56;
 Matches 343; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

QY 118 GAGCCCTCCATCTCCAGGAGATCATGACCCCTTCACCACACAGACACCATCAGACTTAT 177
 Db 1 GAACCTGCTTCTGGGGGAGATAATGGAGACGCACTACGAGAGACACCAACCGACCTAC 60
 QY 178 GTTAACGGCTCAACGCTCCGAGGAGACTACTCGCGCTGTGGCAAGGAGATGTG 237
 Db 61 GTCAACAACCTGAACCGCGGGAGGACAACTGATCAGCGCTTCCGCGAGAGAGCCCG 120
 QY 238 CTTACCCAGGTTAAGCTTTCAGTCTGCTCTCAAGTTTCAACGGAGGAGACATCAATCAC 297
 Db 121 CTGGCGAGATTGGCAGCTGAACGCGATCAANTTCTATCGCGGTGGCCACATCACCAC 180

QY 298 TCTCTGTTCTGGAAGAACTTGGCTCCCTATGATCGAGGAGGCTACCCCTCTCTGAAGGA 357
 Db 181 TCGCTCTTCTGGAAGAACTTGGCTCCCTATGATCGAGGAGGCTACCCCTCTCTGAAGGA 357
 QY 358 CTTCTCAAGAAGGCTATCGAGGAATCTTTTGGTCTTTTCGAGGCTTCAAGAAGAGTTTC 417
 Db 241 GAGCTGGCTCGCGATCGACCGGACTTTGGCTCGGTCGAGCCATGAAGGAGAGTTTC 300
 QY 418 AACGCTGACACCGCTGCTGCTTCAAGGATCGGATGGGCTGGCTTGGCTTGAACCGCTT 477
 Db 301 AACGCGCGCTCGCGGATCATCAGGCTATCGGCTGGGCTGGCTGGGCTGAAACCCACG 360
 QY 478 ACTAAGAAGCTGAAAGTCAACACGACCGCAACACGACCCCTCTGCTTACTCATCTCT 537
 Db 361 ACGGAGAGCTGACATCATCAGCAGCGGACACGAGACCCGCTCTCTGTCGACAGCG 420
 QY 538 ATCATCGGAGTTGACATCTGGGAGCAGCGCTTTCTACTTTCAGTACAGAACGCTCAAGCT 597
 Db 421 CTGATTGGCATCGATCGGTGGGAGCAGCGTACTACCTGAGTACAAAGAACGTCAGGCG 480
 QY 598 GACTATCTCGCTGCTGTTGGTCCGTTATCAACTCAAGGAGCAGAGCCCGGATTCGAG 657
 Db 481 GACTACTTCAAGGCGATCTGGACCGTGATCAACTTTGAGGAGCGCGAGAGCGTCTCANG 540
 QY 658 GCTGCTCTC 666
 Db 541 GAGGCGCTC 549

RESULT 4
 ADD35245
 ID ADD35245 standard; DNA; 897 BP.
 XX AC ADD35245;
 XX 15-JAN-2004 (first entry)
 XX Mouse mitochondrial DNA sequence SEQ ID NO:3025.
 DE ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
 KW mitochondrial disease; oxidative phosphorylation dysfunction;
 KW oxidative stress; apoptosis; aging.
 XX Mus musculus.
 OS WO2003020220-A2.
 PN 13-MAR-2003.
 XX 30-AUG-2002; 2002WO-US027886.
 XX 30-AUG-2001; 2001US-0316323P.
 PR 31-AUG-2001; 2001CA-02356540.
 XX (UYEM-) UNIV EMORY.
 XX Wallace DC, Levy S, Kerstann K, Procaccio V;
 XX WPI; 2003-300821/29.
 XX Array containing probes for genes involved in mitochondrial biology,
 PT useful for determining mitochondrial biology gene expression profiles for
 PT use in diagnosing pathologies and identifying biochemical pathways.
 XX Claim 2; SEQ ID NO 3025; 201pp; English.
 XX The invention relates to a novel array comprising at least two isolated
 CC nucleotide molecules, each molecule having a sequence capable of uniquely
 CC hybridising to a nucleic acid molecule which is an expression product of
 CC a gene involved in mitochondrial biology. The array comprises two or more
 CC isolated nucleic acid molecules or spots, each molecule having a sequence
 CC chosen from sequence of 994 human probes and 2046 mouse probes. An array

of the invention is useful for determining an expression profile of a mouse or human sample containing nucleic acid, by contacting the array with the sample under conditions allowing selective hybridisation, and measuring hybridisation of nucleic acid in the sample to the array to produce an expression profile. The array is also useful for determining an expression profile of a first labelled sample containing nucleic acid relative to a second, differently labelled sample containing nucleic acid. The second sample is a reference or a standard. An array is useful for determining an expression profile diagnostic of an energy-metabolism-related physiological condition. An array of the invention is useful for determining mitochondrial biology gene expression profiles of organisms, such as human, mice and closely related species, tissue and organs of such organisms, which are useful for determining expression profiles diagnostic of energy metabolism-related physiological conditions, identifying such physiological conditions, identifying biochemical pathways, genes, and mutations involved in such physiological conditions, identifying therapeutic agents useful for preventing and/or treating such physiological conditions, evaluating and/or monitoring the efficacy of such therapies, and creating and identifying animal models of human energy metabolism-related physiological conditions. An array is also useful for defining expression signatures or profiles for mitochondrial diseases, as well as distinguishing clinical disorders that result from oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress, apoptosis and aging. An array of the invention contains probes of genes not previously recognised to participate in mitochondrial biology. The sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA clones used to make the probes of the invention. Some sequences are not present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905, 1906, 2408 and 2643.

Seq Sequence 897 BP; 225 A; 214 C; 247 G; 211 T; 0 U; 0 Other;

Query Match 31.6%; Score 211.4; DB 9; Length 897;
Best Local Similarity 63.2%; Pred. No. 1.5e-53;
Matches 367; Conservative 0; Mismatches 196; Indels 18; Gaps 2;

69 CAGGCAAGATACCTGCTGAGCTGCTTACGCTTACGATGCGCTGGAGCCCTCCAT 128
118 CCGGCACAGCAGCAGCTCCAGAGCTGCTTACGACTATGCGCGCTGGAGCCACAT 177
129 CTCACAGGAGATCATGACCTTCCACACCAAGCACCATCAGCTTATGTTAAGCGCT 188
178 TAACGGCAGATCATGAGCTGCACACAGCAGCAGCAGCTGCGCTTACGTTAAACCT 237
189 CAACGCTCCGAGGAGCTACTCGCGCTGTGGGCAAGGAGGATGTGCTTACCCAGGT 248
238 CAACGCCACCGAGGAGATACACAGGCTCTGSCCAAGGAGATGTTACACTCAGT 297
249 TAAGCTTCACTGCTCTCAAGTTCAACGAGGAGGACATCATCACTCTCTGTTCTG 308
298 CGCTCTTCAAGCTGACCTGAAGTTCAATGGTGGGGACATATATACACCACTTTCTG 357
309 GAAGAACTTGGCTCCTATGATCGAGGAGCTACCTCTCTGAGGACCTTCAAGAA 368
358 GACAACTTGAAGCTTGAAGTGTGGAGAACCTT-----AAGGAGTGTCTGGA 408
369 GCTATCGAGGAATCTTTTGGTCTTTTCGAGGCTTCAAGAGAGTTCAAGCTGACAC 428
409 GCTATCAAGCTGACTTTTGGTCTTTTGAAGAGTTTAAAGGAGAGCTGACAGCATGTC 468
429 CGCTGCTTCCAGATCCGATCGGCTGCTGCTGCTGCTGCTGCTGCTTCAAGAGCT 488
469 TGTGGAGTCCAGGTTTCAAGCTGCGGCTGCTGCTGCTGCTTCAATGAAGGAGTGTGCTT 528
489 GGAAGTCCACAGCAGCGCAACAGGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTT 539
529 ACAGATTGCTGCTGCTTATATCAGGACCTTGAAGGAAACAGGCTTATTCGCT 588
540 CATCGAGTTGATCTGGAGCAGCTTTTCTACCTTCAAGTACAGAGCTCAAGCTGGA 599
599 GCTGGGATTCAGCTGCTGGAGCAGCTTACTACCTTCAAGTATATAAAGCTGAGCTGA 648
600 CTAATCCTGCTGTTTGGTTCGCTTATCACTACAGGAGG 640

Db 649 CTATCTGAAGCTATTGGAATGTAATCACTGGGAGATG 689
RESULT 5
ABK63720
ID ABK63720 standard; cDNA; 1492 BP.
AC ABK63720;
XX
DT 18-JUN-2002 (first entry)
XX
DE Rat sequence differentially expressed in response to a hepatotoxin #1627.
XX
KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
KW differential expression; centrilobular necrosis; steatosis.
XX
OS Rattus norvegicus.
XX
PN WO200210453-A2.
XX
PD 07-FEB-2002.
XX
XX 30-JUL-2001; 2001WO-US023872.
XX
XX 31-JUL-2000; 2000US-0222040P.
PR 02-NOV-2000; 2000US-0244880P.
PR 11-MAY-2001; 2001US-0290029P.
PR 15-MAY-2001; 2001US-0290645P.
PR 22-MAY-2001; 2001US-0292336P.
PR 06-JUN-2001; 2001US-0295798P.
PR 13-JUN-2001; 2001US-0297457P.
PR 19-JUN-2001; 2001US-029884P.
PR 09-JUL-2001; 2001US-0303459P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
XX WPI; 2002-241625/29.
XX
XX Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells.
XX
XX Claim 1; SEQ ID NO 1627; 239pp; English.
XX
XX The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The method can also be used to identify an agent which modulates the toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information, identifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the

CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity is
 CC characterised by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent
 XX
 SQ Sequence 1492 BP; 380 A; 328 C; 392 G; 392 T; 0 U; 0 Other;

Query Match 30.6%; Score 205; DB 6; Length 1492;
 Best Local Similarity 62.5%; Pred. No. 1.7e-51;
 Matches 363; Conservative 0; Mismatches 200; Indels 18; Gaps 2;
 QY 69 CAGGGCAAGCATACCTGCTGAGCTTCTTACGCTTACGATCCCTGGAGCCCTCCAT 128
 Db 134 CCGCACAAGCAGCTCCCTGCTTACGCTTACGATGCGGCTGGAGCGGCACAT 193
 QY 129 CTCGAAGGAGATCATGACCTTCCACCAACCAAGCAGCAGCAGCAGCAGCAGC 188
 Db 194 TAACGGCAGATCATGACGCTGCACCAAGCAGCAGCAGCAGCAGCAGCAGCAGT 253
 QY 189 CAACGCTGCCGAGGAGAGCTACTCGCGGCTGTGGCAAGGAGGATGCTTACCCAG 248
 Db 254 GAACGTCACCGAGGAGAGTACCAAGGAGGCTGGCCAAAGGAGATGTTACACTCAG 313
 QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGAGCAGATCAATCACTCTGT 308
 Db 314 TGCTCTTACGCTGCATGAGTTCAATGCGGGGGCCATATCAATCACAGCATTTCT 373
 QY 309 GAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCCCTCTCTGAAGGAGCTCT 368
 Db 374 GACAACTGAGCCCTAAGGCTGTGGAGAACCCCA-----AAGGAGATTGCTGGA 424
 QY 369 GGCTATCGAGAACTTTTGGTCTTTCAGGCGCTTCAAGAGAGTTCAACGCTGACAC 428
 Db 425 GGCTATCAAGCGTGACTTTGGTCTTTTGAAGTTTAAAGAGAACTGACAGCTGTGC 484
 QY 429 CGCTGCTGCCAGGATCCGATCGGCTGTGGCTTGAACCGCTTACTAAGAAAGCT 488
 Db 485 TGTGGAGTCCAGGTTACGCTGGGCTGGCTTGGCTTCAATGAAGAGCAAGTCTGCT 544
 QY 489 GGAAGTCAACCAAGCCGCAACGAGGAGGCTTCTCTCAAGGAGCTCTCAAGAA 539
 Db 545 ACAGATTGCGGCTGCTTAATCAGGACCCCACTCAAGGAGCAGCAGGCTTATTC 604
 QY 540 CATCGGAGTTGACATCTGGAGCAGCTTTTCTAGCTTCAAGAGCAGTCAAGCCTGA 599
 Db 605 GCTGGGATGATGTGTGGGAGCAGCTTACTATCTTCAATATAAAGCAGTCAAGCTGA 664
 QY 600 CTATCTCGCTGCTTGTGGTCCGTTATCAACTACAAGGAGG 640
 Db 665 CTATCTGAAGCCATTGGATGTAACTAAGGAGATG 705

RESULT 6
 ADB58236
 ID ADB58236 standard; DNA; 1492 BP.
 XX
 AC ADB58236;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Toxicity-related gene, SEQ ID 3262.
 XX
 KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;
 KW drug screening; toxicity assay; ds.
 XX
 OS Unidentified.
 XX
 EN WO2003064624-A2.
 XX
 PD 07-AUG-2003.
 XX
 PF 31-JAN-2003; 2003WO-US003194.

XX 31-JAN-2002; 2002US-00060087.
 PR 15-MAR-2002; 2002US-0364045P.
 PR 15-MAR-2002; 2002US-0364055P.
 PR 30-DEC-2002; 2002US-0436643P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
 XX WPI; 2003-689530/65.
 DR
 XX
 PT Predicting a toxic effect of a compound, useful in identifying toxicity
 PT markers in liver tissues or cells for drug screening and toxicity assays,
 PT comprises preparing gene expression profile of tissue or cells exposed to
 PT the compound.
 XX
 PS Claim 1; SEQ ID NO 3262; 1156pp; English.
 XX
 CC The present invention relates to a method for predicting a toxic effect
 CC of a compound. The method comprises preparing a gene expression profile
 CC of a tissue or cell sample exposed to the compound, and comparing the
 CC gene expression profile to a database comprising SEQ ID 1-4925, where
 CC differential expression of the gene indicates at least one toxic effect.
 CC The method is useful for predicting at least one toxic effect of a
 CC compound, predicting hepatotoxicity or the progression of a toxic effect
 CC of a compound, identifying an agent that modulates the onset or
 CC progression of a toxic response, predicting the cellular pathways that a
 CC compound modulates in a cell, and identifying an agent that modulates at
 CC least one activity of a protein. The method and compositions of the
 CC present invention using a database of genes having liver toxin-induced
 CC differential expression, are useful in identifying toxicity markers in
 CC liver tissues or cells for drug screening and toxicity assays. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1492 BP; 380 A; 328 C; 392 G; 392 T; 0 U; 0 Other;

Query Match 30.6%; Score 205; DB 9; Length 1492;
 Best Local Similarity 62.5%; Pred. No. 1.7e-51;
 Matches 363; Conservative 0; Mismatches 200; Indels 18; Gaps 2;
 QY 69 CAGGGCAAGCATACCTGCTGAGCTTCTTACGCTTACGATCCCTGGAGCCCTCCAT 128
 Db 134 CCGCACAAGCAGCTCCCTGCTTACGCTTACGATGCGGCTGGAGCGGCACAT 193
 QY 129 CTCGAAGGAGATCATGACCTTCCACCAACCAAGCAGCAGCAGCAGCAGCAGC 188
 Db 194 TAACGGCAGATCATGACGCTGCACCAAGCAGCAGCAGCAGCAGCAGCAGCAGT 253
 QY 189 CAACGCTGCCGAGGAGAGCTACTCGCGGCTGTGGCAAGGAGGATGCTTACCCAG 248
 Db 254 GAACGTCACCGAGGAGAGTACCAAGGAGGCTGGCCAAAGGAGATGTTACACTCAG 313
 QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGAGCAGATCAATCACTCTGT 308
 Db 314 TGCTCTTACGCTGCATGAGTTCAATGCGGGGGCCATATCAATCACAGCATTTCT 373
 QY 309 GAAGAACTTGGCTCCCTATGGATCCGAGGAGGCTACCCCTCTCTGAAGGAGCTCT 368
 Db 374 GACAACTGAGCCCTAAGGCTGTGGAGAACCCCA-----AAGGAGATTGCTGGA 424
 QY 369 GGCTATCGAGAACTTTTGGTCTTTCAGGCGCTTCAAGAGAGTTCAACGCTGACAC 428
 Db 425 GGCTATCAAGCGTGACTTTGGTCTTTTGAAGTTTAAAGAGAACTGACAGCTGTGC 484
 QY 429 CGCTGCTGCCAGGATCCGATCGGCTGTGGCTTGAACCGCTTACTAAGAAAGCT 488
 Db 485 TGTGGAGTCCAGGTTACGCTGGGCTGGCTTGGCTTCAATGAAGAGCAAGTCTGCT 544
 QY 489 GGAAGTCAACCAAGCCGCAACGAGGAGGCTTCTCTCAAGGAGCTCTCAAGAA 539

Db 545 ACAGATTGGCGCTGCTCTAATCAGGACCACTGCAAGGAACACACAGGCGTTATTCCACT 604
 QY 540 CATCGGAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAAGAGCTCAAGCGCTGA 599
 Db 605 GCTGGGATGATGTGGGAGCACGCTTACTATCTTCAGTATAAAAACGTCAGACCTGA 664
 QY 600 CTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGG 640
 Db 665 CTATCTGAAAGCCATTGGAAATGTAATCAACTGGGAGATG 705

RESULT 7

AAA75734
 ID AAA75734 standard; DNA; 1438 BP.

XX AC AAA75734;

XX DT 22-JAN-2001 (first entry)

XX DE Nucleotide sequence of a manganese superoxide dismutase (Mn SOD).

XX KW Adeno-associated virus; catalase; superoxide dismutase; demyelination;
 KW optic nerve; reactive oxygen species; optic neuritis; optic disk edema;
 KW demyelinating disease; allergic encephalomyelitis; multiple sclerosis;
 KW allergic encephalomyelitis; blood brain barrier; ss.

XX OS Synthetic.

XX PN WO200054595-A1.

XX PD 21-SEP-2000.

XX PF 15-MAR-2000; 2000WO-US006839.

XX PR 15-MAR-1999; 99US-0124398P.

XX PA (GUYJ/) GUY J.

XX PA (QIXX/) QI X.

XX PA (HAUS/) HAUSWIRTH W W.

XX PI Guy J, Qi X, Hauswirth WW;

XX DR WPI; 2000-618854/59.

XX Use of recombinant adeno-associated virus composition for treating
 PT demyelinating disorders e.g. multiple sclerosis and allergic
 PT encephalomyelitis, comprises viral constructs expressing catalase or
 PT superoxide dismutase.

XX PS Disclosure; Page 75-76; 78pp; English.

XX CC The specification describes the use of a recombinant adeno-associated
 CC virus (rAAV) composition. The rAAV comprises a polynucleotide sequence
 CC encoding a mammalian catalase or superoxide dismutase polypeptide to
 CC reduce demyelination in an optic nerve. The rAAV are useful for
 CC scavenging reactive oxygen species in a mammal suspected of having optic
 CC neuritis, to reduce the effects of demyelinating disease in a mammal and
 CC prophylactically used to suppress blood brain barrier disruption in a
 CC mammal having identified allergic encephalomyelitis. The rAAV composition
 CC is useful for reducing symptoms associated with demyelinating diseases
 CC such as optic neuritis, multiple sclerosis, allergic encephalomyelitis,
 CC where the symptoms associated with these disease include optic disk
 CC edema, increase of optic nerve cell count, disruption of blood brain
 CC barrier integrity, increased levels of hydrogen peroxide and
 CC demyelination of axons. The present sequence is expressed using the rAAV
 CC of the invention

XX SQ Sequence 1438 BP; 371 A; 315 C; 368 G; 384 T; 0 U; 0 Other;

Query Match 30.4%; Score 203.4; DB 3; Length 1438;

Best Local Similarity 62.3%; Pred. No. 5.1e-51;

Matches 362; Conservative 0; Mismatches 201; Indels 18; Gaps 2;

QY 69 CAGGGCAAGCATACCTGCTGAGCTTCTTACGCTTACGATGCGCTGAGCGCTCCAT 128
 Db 77 CCGGCACAGACAGACCTCTCTGAGCTGCTTACGACTATGGCGCTGGAGCGCACAT 136
 QY 129 CTCGAAGGAGATCATGACCTTCCACACCAAGCAACCAATCATGACTTATTAACGGCCT 188
 Db 137 TAACGGCAGATCATGAGCTGCACACAGCAAGCACACCGGACCTAGCTGAACAATCT 196
 QY 189 CAACGCTGCGGAGGAGCTACTCGCGCTGCGCAAGGAGGAGTGTCTTACCAGGT 248
 Db 197 GAACGTCACCGAGGAGAGTACCAAGGCGCTGGCCAAAGGAGATGTTACAACCTCAGGT 256
 QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTTCTG 308
 Db 257 TGCTCTTCAGCTGCACCTCAAGTTCAATGCGGGGGCCATATCAATCACAGCATTTCTG 316
 QY 309 GAAGAACTTGGCTCCCTATGATGATCCGAGGAGGCTACCTCTCTGTAAGGACCTCTCAAGAA 368
 Db 317 GACAAACCTGAGCCCTAAGGTGGTGGAGAACCCCA-----AAGGAGAGTTGCTGGA 367
 QY 369 GGTATCGAGGAATCTTTTGGTCTTTTCGAGGCTTCAAGAGAGTTCAGCGCTGCAC 428
 Db 368 GGTATCAAGCGTGACTTTGGGTCTTTTGAAGAGTTTAAGGAGAACTGACAGCTGTGC 427
 QY 429 CGCTGCTGCCAAGGATCCGATCGGCTGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAAGCT 488
 Db 428 TGTGGGAGTCCAAGGTTTCAAGGCTGGGCTGGCTTGGCTTCAATAGGAGCAAGGTCGCT 487
 QY 489 GGAAGTCAACAGCAGCGGCAACAGGACCTCTGC-----TTACTCACATTCCTAT 539
 Db 488 ACAGATTGCGGCTGCTCTTAATCAGAACCCACTGCAAGGAAACACACAGGCTTATTCACCT 547
 QY 540 CATCGAGTTGACATCTGGGAGCAGCTTTTACCTTCAAGTACAGAAAGTCAAGCGCTGA 599
 Db 548 GCTGGGATGATGTGTGGGAGCAGCTTACTATCTTCACTATATAAAACGTGAGACCTGA 607
 QY 600 CTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGG 640
 Db 608 CTATCTGAAAGCCATTGGAAATGTAATCAACTGGGAGATG 648

RESULT 8

AA81158

ID AA81158 standard; cDNA; 813 BP.

XX AC AA81158;

XX DT 22-OCT-1990 (first entry)

XX DE cDNA encoding human manganese superoxide dismutase.

XX KW Human manganese superoxide dismutase; ds cDNA; oxygen free radicals.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 43..711

XX FT /*tag= a

XX PN EP284105-A.

XX PD 28-SEP-1988.

XX PF 25-MAR-1988; 88EP-00104880.

XX PR 27-MAR-1987; 87US-00032734.

XX PR 26-FEB-1988; 88US-00161117.

XX PA (BIOT-) BIO-TECHNOLOGY GEN.

XX PI Hartman JR, Beck Y, Nimrod A;

XX DR WPI; 1988-272584/39.

DR P-PSDB; AAP80551.
 XX Recombinant human manganese superoxidodismutase - used for treating e.g.
 PT reperfusion injury, inflammation, arthritis, bronchial pulmonary
 PT dysplasia or lung fibrosis.
 XX Disclosure; Page ?; 46pp; English.
 XX The cDNA encodes human manganese superoxide dismutase, and is inserted
 CC into a plasmid, eg pMSE-4 (ATCC 53250)
 XX
 XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;
 SQ

Query Match 29.8%; Score 199.4; DB 1; Length 813;
 Best Local Similarity 61.1%; Pred. No. 6.4e-50;
 Matches 367; Conservative 0; Mismatches 216; Indels 18; Gaps 2;

QY 69 CAGGGCAAGCATACCTCGCTGAGCTTCTTACGCTTACGATGCCCTGAGCCCTCCAT 128
 Db 108 CAGGAGAGCAGAGCTCCCGACCTGCCCTACGACTACGGCGCCCTGGAACCTCACAT 167
 QY 129 CTCGAAGGAGATCATGACCCCTTCCACACCAAGCACCATCAGACTATGTTAACGGCCT 188
 Db 168 CAACGGCGAGATCATGAGCTGCACACAGACAGCACACGGCGCCCTACCTGACACACCT 227
 QY 189 CAACGCTGCGAGGAGAGCTACTCGGCCCTGTGGCGAAGGAGATGCTTACCCAGGT 248
 Db 228 GAACGTCACCGAGGAGAGATGACCGAGGAGGCTTGGCCCAAGGAGATGTTACAGCCAGAT 287
 QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCACCGAGGAGGACACATCAATCACTCTCTGTCTG 308
 Db 288 AGCTCTTCAGCTGCATGAGTTCATGTTGGTGGTTCATATCAATCATAGCAATTTCTG 347
 QY 309 GAAGAACTTGGCTCCCTATGATCCGAGGAGGTACCCCTCTCTGAAGGACCTCTCAGAA 368
 Db 348 GACAAACCTCAGCCCTTAACGGTGGTGGAGAACCA-----AAGGGAGTTGCTGGA 398
 QY 369 GGCTATCAGGAATCTTTTGGTCTTTTCAGGCGCTTCAAGNAGAGTTCACGCTGCAC 428
 Db 399 AGCCATCAACAGTGAATTTGGTTTCCCTTGAACAAAGTTAAGGAGAGCTGACGGCTGATC 458
 QY 429 CGCTGCTGTCACAGGATCCGGATGGGCTGGCTTGGCTTGAACCGCTTACTAAGAGCT 488
 Db 459 TGTTGGTGTCCAGGCTCAGTTGGGTTGGCTTGGTTTCAATAAGCAACGGGACACTT 518
 QY 489 GGAAGTCACCAACGACCGCCACACGAGGACCTCTGC-----TTACTCACATTTCCAT 539
 Db 519 ACAAATTTGCTGTTGTCCAAATCAGGATCCACTGCAAGGAAACACAGGCCCTTATCCACT 578
 QY 540 CATCGGAGTTGACATCTGGGAGCAGCGCTTTCTACCTTCAGTACAGAACGTCAGCCCTGA 599
 Db 579 GCTGGGAGTTGATGTGTGGGAGCAGCGTTACTACTCTCAGTATAAATGTGAGGCCCTGA 638
 QY 600 CTATCTCGCTGCTCTTTGGTCCGTTATCAACTACAGGAGGACAGGCCCGAATGACGGC 659
 Db 639 TTATCTAAAGCTATTGGATGTAATCACTGGGAGATGTAATGAAAGATACATGGC 698
 QY 660 T 660
 Db 699 T 699

RESULT 9
 AAQ53193
 ID AAQ53193 standard; cDNA; 813 BP.
 XX
 XX
 AC AAQ53193;
 XX
 XX 25-MAR-2003 (revised)
 DT 21-JUN-1994 (first entry)
 XX
 XX
 DE MnSOD cDNA.
 XX

MnSOD; manganese superoxide dismutase; N-terminal; catalyt; reperfusion;
 injury; ischaemia; superoxide; SO; molecular oxygen; anti-inflammatory;
 ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH 43..711
 FT /*tag= a
 FT /product= "MnSOD"
 XX
 XX US5270195-A.
 XX 14-DEC-1993.
 XX 10-JUL-1992; 92US-00912213.
 XX 22-NOV-1985; 85US-00801090.
 PR 12-SEP-1986; 86US-00907051.
 PR 29-OCT-1986; 86IE-00002851.
 PR 27-MAR-1987; 87US-00032734.
 PR 13-DEC-1989; 89US-00453057.
 XX
 XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
 XX Beck Y, Hartman JR;
 XX WPI; 1993-404931/50.
 DR P-PSDB; AAR44801.
 XX Expression plasmid in Escherichia coli host system - encodes human
 PT manganese superoxidodismutase analogue, useful for e.g. treating
 PT inflammation.
 XX Claim 1; Fig 1a-1c; 27pp; English.
 XX The sequence encodes a manganese superoxide dismutase which can be used to
 CC catalyse the reduction of superoxide (SO) radicals to hydrogen peroxide
 CC and molecular oxygen. It can be used to reduce reperfusion injury
 CC following ischaemia and prolong the survival of excised organs. It can
 CC also be used as a long acting anti-inflammatory drug. (Updated on 25-MAR-
 CC 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
 XX
 XX Sequence 813 BP; 218 A; 203 C; 214 G; 178 T; 0 U; 0 Other;

Query Match 29.8%; Score 199.4; DB 2; Length 813;
 Best Local Similarity 61.1%; Pred. No. 6.4e-50;
 Matches 367; Conservative 0; Mismatches 216; Indels 18; Gaps 2;

QY 69 CAGGGCAAGCATACCTCGCTGAGCTTCTTACGCTTACGATGCCCTGAGCCCTCCAT 128
 Db 108 CAGGAGAGCAGAGCTCCCGACCTGCCCTACGACTACGGCGCCCTGGAACCTCACAT 167
 QY 129 CTCGAAGGAGATCATGACCCCTTCCACACCAAGCACCATCAGACTATGTTAACGGCCT 188
 Db 168 CAACGGCGAGATCATGAGCTGCACACAGACAGCACACGGCGCCCTACCTGACACACCT 227
 QY 189 CAACGCTGCGAGGAGAGCTACTCGGCCCTGTGGCGAAGGAGATGCTTACCCAGGT 248
 Db 228 GAACGTCACCGAGGAGAGATGACCGAGGAGGCTTGGCCCAAGGAGATGTTACAGCCAGAT 287
 QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCACCGAGGAGGACACATCAATCACTCTCTGTCTG 308
 Db 288 AGCTCTTCAGCTGCATGAGTTCATGTTGGTGGTTCATATCAATCATAGCAATTTCTG 347
 QY 309 GAAGAACTTGGCTCCCTATGATCCGAGGAGGTACCCCTCTCTGAAGGACCTCTCAGAA 368
 Db 348 GACAAACCTCAGCCCTTAACGGTGGTGGAGAACCA-----AAGGGAGTTGCTGGA 398
 QY 369 GGCTATCAGGAATCTTTTGGTCTTTTCAGGCGCTTCAAGNAGAGTTCACGCTGCAC 428
 Db 399 AGCCATCAACAGTGAATTTGGTTTCCCTTGAACAAAGTTAAGGAGAGCTGACGGCTGCATC 458

QY 249 TAAGCTTCAGTCTGCTCAAGTTCACGAGGAGGACATCAATCACTCTCTGTTCTG 308
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 Db 399 AGCCATCAACGCTGACTTTGGTCCCTTGACAAGTTTAAAGAGAGCTGACGCTGCATC 458
 QY 429 CGCTGCTGTCAGGATCCGATGGGCTGGCTTGAACCCGCTTACTAAGAGCT 488
 Db 459 TGTGTGTGTCACAGGCTCAGTTGGGCTGGCTTGAATGTAATCAATGAACACGGGACACTT 518
 QY 489 GGAAGTCAACACCGCCCAACAGGACCTCTGC-----TTACTCACATTCCTAT 539
 Db 519 ACAATTTGCTGTGTCTCAATCAGGATCCACTGCAAGGACACAGGCTTATTCACCT 578
 QY 540 CATCGAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGCTCAAGCTGA 599
 Db 579 GCTGGGAGTTGATGTGTGGGAGCACGCTTACTACTTCACTATAAATAATGTCAAGGCTGA 638
 QY 600 CTATCTCGCTGCTTGTGGTCCGTTATCAACTACAAGAGGAGGAGCCCGGCTGAGGC 659
 Db 639 TTATCTAAAAGCTATTGGAATGTAATCAACTGGGAGATGTAATCTGAAAGATACATGGC 698
 QY 660 T 660
 Db 699 T 699

RESULT 14
 ID AAN71370 standard; DNA; 813 BP.
 AC AAN71370;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)
 DT 14-MAY-1991 (first entry)
 XX
 DE Sequence encoding human manganese superoxide dismutase.
 XX
 KW Human MSOD; hydrogen peroxide; ischaemia; lesions; inflammation;
 KW free radicals; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 43..711
 FT /*tag= a
 FT 115..708
 FT /*tag= b
 FT /product= "mature MSOD"
 XX
 PN BE905796-A.
 XX
 PD 16-MAR-1987.
 XX
 PF 20-NOV-1986; 86BE-00905796.
 XX
 PR 22-NOV-1985; 85US-00801051.
 PR 22-NOV-1985; 85US-00801090.
 PR 12-SEP-1986; 86US-00907051.
 XX
 FA (BIOT-) BIO-TECHNOL GEN.
 XX
 DR WPI; 1987-101441/15.
 DR P-PSDB; AAP71370.
 XX

PT New DNA coding for polypeptide of human manganese superoxidizedismutase -
 PT useful e.g. for treating inflammation, and new expression vectors and
 PT transformed cells.
 XX Disclosure; Fig 1; 46pp; French.
 XX This purified cDNA encodes both prepro- and mature-manganese superoxide
 CC dismutase (MSOD). It is one strand of a double stranded molecule
 CC contained in a recombinant vehicle. The MSOD produced catalyses the
 CC reaction of hydrogen ions and the SOD radical anion to form hydrogen
 CC peroxide and water. It is useful in veterinary and pharmaceutical
 CC compans. for e.g. reducing lesions of reperfusion following ischaemia, to
 CC prolong survival time isolated organs and for treating inflammation. See
 CC also AAN71371-72. (Updated on 10-MAR-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 813 BP; 218 A; 204 C; 213 G; 178 T; 0 U; 0 Other;
 Query Match 29.6%; Score 197.8; DB 1; Length 813;
 Best Local Similarity 60.9%; Pred. No. 2e-49;
 Matches 366; Conservative 0; Mismatches 217; Indels 18; Gaps 2;
 QY 69 CAGGGCAAGCATPACCTGCTGAGCTTCCTTACGTTAGATGCCCTGAGCCCTCCAT 128
 Db 108 CAGGCAAGACACAGGCTCCCGACCTGCCCTACGACTACGGCGCCCTGGAACCTCAT 167
 QY 129 CTCAGAGGATCATGACCTTCACACACCAAGCACCATCAGACTTATGTTAAGCCCT 188
 Db 168 CACCGGCGAGTATGAGCTGCACACACAGCAGCACCACGCGGCTTACGTGAACACCT 227
 QY 189 CAACGCTGCCGAGGAGAGCTACTCGGCGCTGTGGCAAGGAGGATGTGTTACCCAGGT 248
 Db 228 GAACGTCAACGAGGAGAGTACCAGGAGGCGTTCGCCAAGGAGATGTTACAGCCACAT 287
 QY 249 TAAGCTTCAGTCTGCTTCAAGTTCAACGAGAGAGACATCATCACTCTCTGTTCTG 308
 Db 288 AGCTCTTCAGCTGCACCTGAAGTTCAATGGTGGTGCATATCAATCATAGCAATTTCTG 347
 QY 309 GAAGAACTTGGCTCCCTATGATCCGAGGAGGCTACCTCTCTCAAGGACCTCTCAAGAA 368
 Db 348 GACAACTCAGCCCTAACGCTGAGAACCA-----AAGGGAGTTGCTGGA 398
 QY 369 GGTATCGAGGAATCTTTGGTCTTTCGAGGCTTCAAGAAAGTTCAACGCTGACAC 428
 Db 399 AGCCATCAACGCTGACTTTGGTCCCTTGACAAGTTTAAAGAGAGCTGACGCTGCATC 458
 QY 429 CGCTGCTGTCAGGATCCGAGTGGGCTGGCTTGAACCCGCTTACTAAGAGCT 488
 Db 459 TGTGTGTGTCACAGGCTCAGTTGGGCTGGCTTGAATGTAATCAATGAACACGGGACACTT 518
 QY 489 GGAAGTCAACACCGCCCAACAGGACCTCTGC-----TTACTCACATTCCTAT 539
 Db 519 ACAATTTGCTGTGTCTCAATCAGGATCCACTGCAAGGACACAGGCTTATTCACCT 578
 QY 540 CATCGAGTTGACATCTGGGAGCACGCTTTCTACCTTCAGTACAAGAACGCTCAAGCCCTGA 599
 Db 579 GCTGGGAGTTGATGTGTGGGAGCACGCTTACTACTTCACTATAAATAATGTCAAGGCTGA 638
 QY 600 CTATCTCGCTGCTTGTGGTCCGTTATCAACTACAAGAGGAGGAGCCCGGCTGAGGC 659
 Db 639 TTATCTAAAAGCTATTGGAATGTAATCAACTGGGAGATGTAATCTGAAAGATACATGGC 698
 QY 660 T 660
 Db 699 T 699

RESULT 15
 ID AEN84891 standard; cDNA; 849 BP.
 AC AEN84891;
 XX
 DR WPI; 1987-101441/15.
 DR P-PSDB; AAP71370.
 XX

DT 15-NOV-2002 (first entry)
 XX Human manganese superoxide dismutase gene.
 XX Superoxide dismutase; SOD; hSODm; enzyme; human; osteopathic;
 KW antirheumatic; antiarthritic; vasotropic; antiinflammatory; gene; ss.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 FT misc_feature 1..8
 FT /tag= a
 FT /note= "EcoRI linker used in cloning"
 FT CDS 100..768
 FT /tag= b
 FT /product= "hSODm"
 FT sig_peptide 100..171
 FT /tag= c
 FT mat_peptide 172..765
 FT /tag= d
 FT misc_feature 842..849
 FT /tag= e
 FT /note= "EcoRI linker used in cloning"
 XX US2002081287-A1.
 PN 27-JUN-2002.
 XX 11-JUN-2001; 2001US-00878589.
 PF 14-OCT-1986; 86US-00918534.
 XX (CHIR) CHIRON CORP.
 XX Hallelwell RA, Bell GI, Mullenbach GT;
 XX WPI; 2002-626527/67.
 DR P-PSDB; ABB79798.
 XX Preparing recombinant human manganese superoxide dismutase, useful in the
 PT treatment of osteoarthritis and rheumatoid arthritis.
 XX Example 1; Fig 4; 16pp; English.
 XX The present sequence is the nucleotide sequence of human manganese
 CC superoxide dismutase (hSODm) cDNA. The cDNA was isolated from an adult
 CC human kidney cDNA library in lambda-gt10 using the probes given in
 CC ABN8489-90. The invention relates to methods for hSODm gene cloning and
 CC expression in microorganisms, especially Escherichia coli or
 CC Saccharomyces cerevisiae. The hSODm cDNA is inserted into a vector for
 CC expression in the microbial host, preferably under conditions which allow
 CC for processing to remove the N-terminal methionine. The expression
 CC product is useful for treating a patient having inflammatory joint
 CC disease (e.g. osteoarthritis or rheumatoid arthritis), or to minimise
 CC post-ischaemic tissue damage resulting from disease or surgery
 XX SQ Sequence 849 BP; 256 A; 197 C; 227 G; 169 T; 0 U; 0 Other;
 Query March 29.6%; Score 197.8; DB 6; Length 849;
 Best Local Similarity 60.9%; Pred. No. 26-49;
 Matches 366; Conservative 0; Mismatches 217; Indels 18; Gaps 2;
 QY 69 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
 Db 165 CAGGCAAGCATACCCCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 224
 QY 129 CTCGAAGGAGATCATGCCCTTCACACACACACACATCAGACTTATGTAAAGGCT 188
 Db 225 CAACGCGAGATCATGCGCTGACACACAGCAAGCAACCGCGGCTACGTGAACAACCT 284
 QY 189 CAACGCTGCCGAGGAGAGCTACTCGCGCTGTGTGGCAAGGAGGATGTCTTACCCAGGT 248
 Db 285 GNAACGTCACGAGGAGAGTACCAAGAGGAGGCTTGGCCCAAGGAGATGTTACAGCCCAT 344

QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTCTG 308
 Db 345 AGCTCTTCAGCTGCACTCAAGTTCAATGGTGGTGGTCAATCAATCAATCAATCAATCA 404
 QY 309 GAAGAACTGGCTCCCTATGGATCCGAGAGGCTACCCCTCTCTGAAGGACCTCTCAAGAA 368
 Db 405 GACAAACCTCAGCCCTAACGGTGGTGGAGAACCCA-----AAGGGGAGTTGCTGA 455
 QY 369 GGTATCGAGGAATCTTTTGGTTCTTTTCGAGGCTTCAAGAAAGATTCAACGCTGACAC 428
 Db 456 AGCCATCAAAACGTGACTTTGGTTCTTTGACAAGTTTAAGGAGAGCTACCGCTGCATC 515
 QY 429 CGCTGCTGTCCAAAGGATCCGGATGGGCTTGGCTTGAACCCGCTTACTAAGAAGCT 488
 Db 516 TGTGGTGTCCAAAGGCTCAGTTGGGTTGGCTTGGTTTCAATAGGAACGGGACACTT 575
 QY 489 GGAAGTCAACGACGCGCAACACGAGGACCTCTGTCTTACT-----CAGATCTCTAT 539
 Db 576 ACAAAATGTGCTTGTCCAAATCAGGATCCACTGCAAGGAAACAACAGGCTTTATTCCACT 635
 QY 540 CATCGAGTTGACATCTGGAGCAGCTTTCTTACCTTCAGTACAAAGAGCTCAAGCTGA 599
 Db 636 GCTGGGATTTGATGTGGGAGCAGCTTACTACCTTCAGTATAAAATGTCAAGGCTGA 695
 QY 600 CTATCTCGTCTGTGTTCGTTTATCAACTACAAAGGAGGAGGAGGAGGAGGAGGAGGAG 659
 Db 696 TTATCTAAAGCTATTTGGAATGTAATCAACTGGGAGATGTAACCTGAAGATACATGCG 755
 QY 660 T 660
 Db 756 T 756

Search completed: April 1, 2004, 13:40:13
 Job time : 262.583 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 12:35:05 ; Search time 2584.54 Seconds
(without alignments)
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Title: US-09-727-855B-4
Perfect score: 669
Sequence: 1 atgtctgttcgagcatccct.....gattgcaggctgctctctaa 669

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.ov.*
- 5: gb.pat.*
- 6: gb.pl.*
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- 13: gb.un.*
- 14: gb.vi.*
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- 17: em.hum.*
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- 20: em.om.*
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- 22: em.ov.*
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- 24: em.ph.*
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- 33: em.htg.mus.*
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- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	669	100.0	669	6	AX128479	Sequence
2	669	100.0	669	6	BD015713	Recombina
3	316.6	47.3	597	6	AX128481	Sequence
4	316.6	47.3	597	6	BD015714	Recombina
5	294	43.9	678	8	AY423629	Cryptococ
6	258.8	38.7	704	8	GMU56403	Ganoderma m
7	252	37.7	728	6	E15568	cdNA encodi
8	252	37.7	728	6	AR222757	Sequence
9	250.6	37.5	812	6	E15569	cdNA encodi
10	250.6	37.5	812	6	AR222758	Sequence
11	246.6	36.9	621	8	AF114848	Paxillus
12	220.6	33.0	630	6	AR222775	Sequence
13	216.8	32.4	629	6	E15585	cdNA encodi
14	214.8	32.1	750	8	MSY548421	Malassezi
15	213	31.8	779	10	MMNSODRX	M.musculus
16	211.4	31.6	897	10	MMNSODR	Mouse mRNA
17	208.2	31.1	836	10	BC018173	Mus muscu
18	208.2	31.1	954	4	AB001693	Equus cab
19	208.2	31.1	1162	10	BC010548	Mus muscu
20	208	31.1	799	8	AY027564	Aspergill
21	207.6	31.0	693	8	AY206454	Cordyceps
22	206	30.8	878	8	R1CSODAOA	Rice mitoch
23	206	30.8	901	8	AK104160	Oryza sat
24	206	30.8	909	8	AK104030	Oryza sat
25	206	30.8	928	8	AK070528	Oryza sat
26	206	30.8	951	8	R1CRMSO	Oryza sativ
27	206	30.8	1352	8	R1CRMSOA	Oryza sativ
28	205	30.6	1492	6	AX401951	Sequence
29	204.4	30.6	901	8	AK119904	Sequence
30	203.4	30.4	1438	10	RNMNSOD	Rat mRNA fo
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36	197.8	29.6	669	12	BT007684	Synthetic
37	197.8	29.6	813	6	EC01408	cdNA encodi
38	197.8	29.6	940	9	BC012423	Homo sapi
39	197.8	29.6	1026	6	AX334340	Sequence
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ALIGNMENTS

RESULT 1	AX128479	669 bp	DNA	linear	FAT 15-MAY-2001
LOCUS	AX128479	Sequence 4 from Patent EP1111067.			
DEFINITION	AX128479				
ACCESSION	AX128479.1	GI:14134946			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
					Xanthophyllomyces dendrorhous (anamorph: Phaffia rhodozyma)
					Xanthophyllomyces dendrorhous
					Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
					Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;
					Cystofilobasidiaceae; Xanthophyllomycetes.
REFERENCE					1
AUTHORS					Hoshino, T., Ojima, K. and Setoguchi, Y.
TITLE					Recombinant production of carotenoids, particularly astaxanthin

JOURNAL	Patent: EP 1111067-A 4 27-JUN-2001; F. HOFFMANN-LA ROCHE AG (CH)
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source	1..669
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	/db_xref="taxon:5421"
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	/note="unnamed protein product"
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ORIGIN	
Query Match	100.0%; Score 669; DB 6; Length 669;
Best Local Similarity	100.0%; Pred. No. 5,3e-168;
Matches 669; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGTCGTGTCGAGCATCCCTCTCTCCGTCGTCTAGACAGACTTCGTCGCTCTGCTGCT 60
Db	1 ATGTCGTGTCGAGCATCCCTCTCTCCGTCGTCTAGACAGACTTCGTCGCTCTGCTGCT 60
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QY	121 CCTCCATCTCAAGGAGATCATGACCTTCCACCAACCAAGCACCATCAGACTTATGTT 180
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QY	241 ACCGAGGTTAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACATCAATCACTCT 300
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Db	661 GCTCTCTTAA 669
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LOCUS	Recombination production of carotenoids, in particular, astaxanthin.
DEFINITION	astaxanthin.
ACCESSION	BD015713
VERSION	BD015713.1 GI:22556850
KEYWORDS	JP 2001190294-A/4.
SOURCE	Xanthophyllomyces dendrorhous (anamorph: Phaffia rhodozyma)
ORGANISM	Xanthophyllomyces dendrorhous
	Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
	Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;
	Cystofilobasidiaceae; Xanthophyllomyces.
REFERENCE	1 (bases 1 to 669)
AUTHORS	Hoshino,T.; Ojima,K. and Setoguchi,Y.
TITLE	Recombination production of carotenoids, in particular, astaxanthin
JOURNAL	Patent: JP 2001190294-A 4 17-JUL-2001;
COMMENT	F HOFFMANN LA ROCHE AG
	OS Phaffia rhodozyma
	PN JP 2001190294-A/4
	PD 17-JUL-2001
	PF 01-DEC-2000 JP 2000367099
	PR 01-DEC-1999 EP 99123821.3
	PI TATSUO HOSHINO,KAZUYUKI OJIMA,YUTAKA SETOGUCHI PC
	(C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12P23/00,C12O1/68// PC
	(C12P23/00,C12R1/01),(C12P23/00,C12R1/18),(C12P23/00,C12R1/20), PC
	(C12P23/00,C12R1/465),(C12P23/00,C12R1/645),C12N15/00 CC
	Recombination production of carotenoids, in particular, CC
	astaxanthin
PH Key	Location/Qualifiers
FT CDS	(1)..(669).
FEATURES	
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	/organism="Xanthophyllomyces dendrorhous"
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ORIGIN	
Query Match	100.0%; Score 669; DB 6; Length 669;
Best Local Similarity	100.0%; Pred. No. 5,3e-168;
Matches 669; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGTCGTGTCGAGCATCCCTCTCTCCGTCGTCTAGACAGACTTCGTCGCTCTGCTGCT 60
Db	1 ATGTCGTGTCGAGCATCCCTCTCTCCGTCGTCTAGACAGACTTCGTCGCTCTGCTGCT 60
QY	61 TTCCAGATCAGGCAAGCATACCTGCTGAGCTTCCTTACGCTTACGATCCCTGGAG 120
Db	61 TTCCAGATCAGGCAAGCATACCTGCTGAGCTTCCTTACGCTTACGATCCCTGGAG 120
QY	121 CCTCCATCTCAAGGAGATCATGACCTTCCACCAACCAAGCACCATCAGACTTATGTT 180
Db	121 CCTCCATCTCAAGGAGATCATGACCTTCCACCAACCAAGCACCATCAGACTTATGTT 180
QY	181 AACGGCTCAAGCTTCCGAGAGAGTACTCGGCGCTGTGGCAAGGAGGATGCTT 240
Db	181 AACGGCTCAAGCTTCCGAGAGAGTACTCGGCGCTGTGGCAAGGAGGATGCTT 240
QY	241 ACCGAGGTTAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACATCAATCACTCT 300
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QY	361 CTGTTCTCGAAGAACTTGGCTTCCATGATCCGAGGAGGCTACCTCTCTGAAAGGCTTACT 420
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QY	421 ATGTCGTGTCGAGCATCCCTCTCTCCGTCGTCTAGACAGACTTCGTCGCTCTGCTGCT 480
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QY	481 AAGAGCTGGAAGTCAACCAAGCAGGACCCCTCTGCTTACTTCAATCTCTATC 540
Db	481 AAGAGCTGGAAGTCAACCAAGCAGGACCCCTCTGCTTACTTCAATCTCTATC 540
QY	541 ATCGAGGTTGACATCTGGAGCAGCTTTTACCTTCACTTCACTTCACTTCACTTCACT 600
Db	541 ATCGAGGTTGACATCTGGAGCAGCTTTTACCTTCACTTCACTTCACTTCACTTCACT 600
QY	601 TATCTCGCTGCTGTTTGGTTCGCTTATCAACTTCAAGGAGGAGGAGGAGGAGGAGGCT 660
Db	601 TATCTCGCTGCTGTTTGGTTCGCTTATCAACTTCAAGGAGGAGGAGGAGGAGGAGGCT 660
QY	661 GCTCTCTTAA 669
Db	661 GCTCTCTTAA 669

Db	232	AGAAACATGGCTCCCTGCGCAGCTCTGCTGAAGCAAGCTCACGAGGATCGCTCAAGACT	291
QY	370	GCTATCGAGGAATCTTTTGGTTCTTTTCGAGGCTTCAAGAGAAAGTTCAACGCTGACACC	429
Db	292	GCCATCGACAAGGACTTTGGATCCCTTCGAGGAGTTCAAGAGAAAGTTCAACACTGCTACT	351
QY	430	GCTGCTGTCGAAGATCCGGATGGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAGCTG	489
Db	352	CTCGGTGTCAGGGATCTGGATGGGATGGCTCGGATCAACAACCCGCTACCAAGCACCTC	411
QY	490	GAAGTCACCAAGCAGCCGACAGGAGCCCTCTGCTTACTCAATTCCTATCATCGGAGTT	549
Db	412	GAGATCGCCACCAACCCGACCAAGGATCCCTTATCACTTGTGATCCCATCTGTCCT	471
QY	550	GACATCTGGGAGCAGCTTTCTACCTTCAGTCAAGAAGCTCAAGCTGACTATCTCGCT	609
Db	472	GACATCTGGGAGCAGCTTCTACCTCCAGTCAAGAAGTGTCAAGCTGATTACCTTGCC	531
QY	610	GCTGTTTGGTCCGTTATCAACTCAAGGAGGAGAGCCCGATGAGGCTGCTCTCTA	668
Db	532	GCTTCTCGAAACGCTGCAACTTTGCTGAGGCTCAGCGAGGTTGATGCTGCTGCAA	590
RESULT 4	BD015714	597 bp DNA linear	PAT 27-AUG-2002
LOCUS	BD015714	Recombination production of carotenoids, in particular, astaxanthin.	
DEFINITION	BD015714	BD015714.1 GI:22556851	
ACCESSION	BD015714	JP 2001190294-A/5.	
VERSION	BD015714	Xanthophyllomyces dendrorhous (anamorph: Phaffia rhodozyma)	
KEYWORDS	BD015714	Xanthophyllomyces dendrorhous	
SOURCE	BD015714	Eukaryota: Fungi: Basidiomycota; Hymenomycetes;	
ORGANISM	BD015714	Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;	
REFERENCE	BD015714	Cystofilobasidiaceae; Xanthophyllomyces.	
AUTHORS	BD015714	1 (bases 1 to 597)	
TITLE	BD015714	Hoshino, T., Ojima, K. and Setoguchi, Y.	
JOURNAL	BD015714	Recombination production of carotenoids, in particular, astaxanthin	
COMMENT	BD015714	Patent: JP 2001190294-A 5 17-JUL-2001;	
	BD015714	F HOFFMANN LA ROCHE AG	
	BD015714	OS Phaffia rhodozyma	
	BD015714	PN JP 2001190294-A/5	
	BD015714	PD 17-JUL-2001	
	BD015714	PF 01-DEC-2000 JP 2000367099	
	BD015714	PR 01-DEC-1999 EP 99123821.3	
	BD015714	PI TATSUO HOSHINO, KAZUYUKI OJIMA, YUTAKA SETOGUCHI PC	
	BD015714	CI2N15/09, CI2N11/15, CI2N11/19, CI2N1/21, CI2P23/00, CI2Q1/68// PC	
	BD015714	(CI2P23/00, CI2R1:01), (CI2P23/00, CI2R1:18), (CI2P23/00, CI2R1:20), PC	
	BD015714	(CI2P23/00, CI2R1:465), (CI2P23/00, CI2R1:645), CI2N15/00 CC	
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source	BD015714	(1)..(597).	
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	BD015714	/db_xref="taxon:5421"	
ORIGIN	BD015714	47.3%; Score 316.6; DB 6; Length 597;	
	BD015714	Best Local Similarity 72.0%; Pred. No. le-73;	
	BD015714	Matches 431; Conservative 0; Mismatches 159; Indels 9; Gaps 1	
QY	70	AGGGCAAGACATPACCTGCTGAGCTTCCTTACGCTTAGATGCGCTGGAGCCCTCCATC	129
Db	1	ATGGCTCCCTTACACTCTTCCGACCTTCTTACGCTTAGATGCGCTGGAGCCTTACATC	60
QY	130	TCAAGGAGATCATGACCTTCCACACACCAAGCACCATCACACTTATCTTAACGGCCTC	189
Db	61	TCTAAGGAATCATGATTCCTTCCACCTCAAGCACCATCACACTTACGTCACCACTTC	120

Qy	190	AACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGCAAGGAGGATGTGCTTACCAGGTT	249
Db	121	AACGCCGCTATCCAGGCTTTCTCCAGACCAATGACATCAAG-----CCAGATC	171
Qy	250	AAGCTTCAGTCTGCTCTCAAGTTCAACGGAGGAGACACATCAATCACTCTCTGTTCGG	309
Db	172	GCTCTTCAAGCGCTCTCAAGTTCAACGGAGGAGACACATCAACCACTCCCTCTCTCG	231
Qy	310	AAGAACTTGGCTCCCTATGSGATCCGAGGAGGCTACCTCTCTGAAGGACCTCTCAAGAAG	369
Db	232	AAGAACTGGTCTCTGCCGACTCTGCTGATGCCAAGCTCACCGAGGATCGTCAAGACT	291
Qy	370	GCTATCGAGGAATCTTTTGGTTCTTTCCAGGCCCTTCAAGAAGATTCAACGCTGACACC	429
Db	292	GCCATCGACAAGGACTTTGGATCCCTTCGAGGAGTTCAAGAAGATTCAACACTGCTACT	351
Qy	430	GTCGCTGTCCAAGGATCCGGATGGGGCTGGCTTGGCTTGAACCGCTTACTAAGAAGCTG	489
Db	352	CTCGGTGTCCAGGGATCTGGATGGGATGGCTCGGATACACACGCTACCAAGCACCTC	411
Qy	490	GAAGTCACCAAGCGGCCAACCAAGGACCTCTGCTTACTCAATTCCTATCATCGGAGTT	549
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Qy	550	GACATCTGGGAGCAGCTTTTCTACCTTCAGTACAAGAACGCTCAAGCCTCGACTATCTCGCT	609
Db	472	GACATCTGGGAGCAGCTTTTCTACCTCCAGTACAAGAAATGTCAAGCCTGATTAACCTTGCC	531
Qy	610	GCTGTTTGTTCGGTTATCAACTACAAGGAGCAGAGGCCCGGATTGCAAGGCTGCTCTCTA	668
Db	532	GCCTTCGGAACGTCCTGCACTTTTGTGAGCTCAGGAAGGTTTGATGTGCTGTCAAA	590

Query Match	43.9%;	Score 294;	DB 8;	Length 678;	
Best Local Similarity	69.0%;	Pred. No. 1.2e-67;			
Matches 418;	Conservative	0;	Mismatches 185;	Indels 3;	Gaps 1
QY	67	ATCAGGGCAAGCATACCTGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCC	126		
DB	73	ATTAGGGCCAGCACACCTTCCCTCTTATGCTACGAGCGGTGAGAGCTTCC	132		
QY	127	ATCTCAAAGGAGTCATGACCCCTTCACCACACCAAGCACCATCAGACTTATGTTAAACGGC	186		
DB	133	ATCTCTTCTGAGATTATGAACCTCCATCACACCAAGCATCACAGACTTACGTTAACGGT	192		
QY	187	CTCAACGCTGCCGAGGAGAGCTACTGCGCGCTGTGGCAAGGAGGATGTGCTTACCCAG	246		
DB	193	CTTAAACGCTGCTGAGGAGTCTCTCAGAAAGCCCTCTGCAGCTGGTACGTTTAAAGCTGCT	252		
QY	247	GTTAAGCTTCAGTCTGCTCTCAAAGTTCAAAGGAGGAGACACATCAATCACTCTCTGTTC	306		
DB	253	ATTGCGCTTCAGCCGCGCCTCAAAATTCAAACGGTGGTGGTCAATTAATCACTCTCTTTC	312		
QY	307	TGGAGAACTTGGCTCCCTATGATTCGAGGAGGCTA---CCCTCTCTGAAAGGACCTGTC	363		
DB	313	TGGAAGAACCCTTGCTTCCACCGGCTCTGCTCAGGTCAGGTTCCGACCTCCGGTGTCTTC	372		
QY	364	AAGAAGGCTATCGAGGAATCTTTTGGTCTTTCGAGGCTTTCAGAGAAGGTTCAAACGCT	423		
DB	373	CATGACCACGTCGAGGCTGACTTTTGGTGGCTTCGAAACCTCAAGAAGGAGTGAATGCC	432		
QY	424	GACACCGCTGTGTCCAAAGATCCGGATGGGGCTGGCTTGGCTTGAACCCGCTTACTAAG	483		
DB	433	AAGACTGTGTGCATCCAAAGGCTCTGGTTGGGGCTGGCTCGGTTTACAACAAGGCAACCAAG	492		
QY	484	AAGCTGGAAGTCAACACAGACCGCAACAGACCCCTCTGCTTACTGCATTCCTTATCATC	543		
DB	493	AAGCTCGAGATTGTACCACTTCCCAATCAGGACCCCTCTTGTGCCACGTCCTTATCAT	552		
QY	544	GGAGTGCATPCTGGGAGCAGCTTTTCTACCTTCAGTACAAGAAGCTCAAAGCCGTGACTAT	603		
DB	553	GGCATTTGACATCTGGGAGCATGCTTTTCTACCTTCAGTACAAGAAGCTCAAAGCCGATTC	612		
QY	604	CTCGCTGCTGTTTGGTCCGTTATCAACTACAAGGAGCAGAGGCCCGGATTCGAGGCTGCT	663		
DB	613	CTCAACGCCATCTGGGACGTTTATCACTACGAGGAGCCGAGAACCGTCTGAAGGCTGCC	672		
QY	664	CTCTAA	669		
DB	673	CTGTGA	678		

GMU56403	704 bp	linear	PLN 04-SEP-1996
LOCUS			
DEFINITION	Ganoderma microsporium manganese-superoxide dismutase mRNA, complete cds.		
ACCESSION	U56403		
VERSION	U56403.1	GI:1519035	
KEYWORDS			
SOURCE	Ganoderma microsporium		
ORGANISM	Ganoderma microsporium		
REFERENCE	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Aphyllophorales; Ganodermataceae; Ganoderma.		
AUTHORS	1 (bases 1 to 704)		
TITLE	Wang,H.-F. and Hseu,R.-S.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (24-APR-1996) Huei-Fang Wang, Applied Microbiology Laboratory/Agricultural Chemistry Department, National Taiwan University, Taipei, Taiwan, Republic of China		
AUTHORS	2 (bases 1 to 704)		
TITLE	Wang,H.-F.		
JOURNAL	Studies of Manganese-Superoxide Dismutase Gene of Ganoderma Thesis (1996) National Taiwan University, Taipei, Taiwan, Republic of China		
FEATURES	Location/Qualifiers		

ORIGIN

FEATURES


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ORIGIN
Query Match 38.7%; Score 258.8; DB 8; Length 704;
Best Local Similarity 68.0%; Pred. No. 3.1e-58;
Matches 400; Conservative 0; Mismatches 167; Indels 21; Gaps 2;

QY 79 CATACCTGCTGAGCTTCCTTACGCTTACGCTGAGCCCTCGAGCCCTCCATCTCCAAAGGAG 138
DB 40 CACGTCTCTCCCGACCTCCGCTAGCGGTACACGCGCTCGAGCCCTTCATCTCGCAGCAG 99

QY 139 ATCATGACCTTCACACACCAAGCACCACATGACATTTATGTTAAGCGCTCAAGCTGCC 198
DB 100 ATCATGAGCTCCACCACCAAGAGCACCACGACCTACGTCACCTCGCTCAAGCGCGCC 159

QY 199 GAGGAGAGTACTCGGCGCTGTGGCAAGGAGATGTGTTACCCAGGTTAAGCTTCAG 258
DB 160 GAGGAGGCTTACGCGCAAGGCTCCACCCCAAGGAGCGCATCGCC-----CTCCAG 210

QY 259 TCTGCTCTCAAGTTCAACGGAGGAGGACACATCAATCACTCTCTGTTCTGGAAGAACTTG 318
DB 211 TCGGCCCTCAAGTTCAACGGCGGTGGTACATCAACCACTCCCTCTTCTGGAAGAACTT 270

QY 319 GTCCTCTATGATCCGAG-----GAGCTACCTCTCTGAAGNACCTCTCAAG 366
DB 271 GCCCGCGCTCAAGTCCGAGGCAAGGCAACGCGCGCGCTCCGCGGAGCGCCCTCAAG 330

QY 367 AAGCTATCGAGGAATCTTTTGGTTCTTCGAGCGCTTCAAGAGAAAGTTCAACGCTGAC 426
DB 331 TCTCGATTCGAGAGAACTGGGGCTCCGTGCAACATTCATCAAGGAGTTCAAGCCACC 390

QY 427 ACCGCTGTGTCGAGGATCCGATGGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAG 486
DB 391 ACTGCTGCATCCAGGGCTCTGGCTGGGGCTGGCTCGGACTTAAACCCGCAACGAGCGT 450

QY 487 CTGGAAGTCAACGACCGCAACGAGACCTCTGTTACTCATCTCATCTTATCATCGGA 546
DB 451 CTCGAGATAACGACCGCCCAATCAGGACCGCTCTCTCGCATGTCCCATCATCGGC 510

QY 547 GTTGACATCTGGGACGCTTTCTACCTTCAGTACAAAGACGTCGAAGCTGACTATCTC 606
DB 511 GTCGATATCTGGAGCAGCGGTTCTACTCTCAGTACTCTCAAGTCAAGCGCGACTACCTG 570

QY 607 GCTGCTGTTGGTCCGTTATCAACTTCAAGGAGGAGGAGGCGGCGGATG 654
DB 571 GCGGCGATCGATCGTGTATCAACTTCAAGGAGGAGGAGGCGTGTGCTG 618

RESULT 7
LOCUS E15568 728 bp DNA linear PAT 28-JUL-1999
DEFINITION cDNA encoding Malassezia antigen protein MF-3.
ACCESSION E15568
VERSION E15568.1 GI:5710251
KEYWORDS JP 1998077296-A/3.
SOURCE unidentified
ORGANISM unidentified.

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REFERENCE
AUTHORS Takesako,K., Daimon,H., Kuroda,M., Katou,I., Yasueda,H., Akiyama,K.
and Yamaguchi,H.
TITLE RECOMBINANT MALASSEZIA ANTIGENIC PROTEIN AND ITS GENE
JOURNAL Patent: JP 1998077296-A 3 24-MAR-1998;
COMMENT TAKARA SHUZO CO LTD
OS Malassezia furfur
PN JP 1998077296-A/3
PD 24-MAR-1998
PP 05-SEP-1996 JP 1996257613
PI TAKESAKO KAZUTADA, DAIMON HISASHI, KURODA MASANOBU, PI KATOU
IKUNOSHIN,
PI YASUEDA HIROSHI, AKIYAMA KAZUO, YAMAGUCHI HIDEYO PC
C07K14/195,A61K39/35,C07H21/04,C07K7/08,C12N15/09,C12Q1/68, PC
G01N33/53,
PC G01N33/569;
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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Best Local Similarity 65.5%; Pred. No. 2e-56;
Matches 385; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 68 TCAGGCAAGGATACCTGCTGAGCTTCCTTACGCTTACGATGCTGAGCCCTGAGCCCTCCA 127
DB 8 TCATGACTGATGATCACTCTCCCTCTCTGCTTACGCTTACGCTGAGCGGTGTTA 67

QY 128 TCTCAAGGAGATCATGACCCCTTCCACACACCAAGCACCATCACTATGTTAAAGGCC 187
DB 68 TCTCTAAGGAGATCATGAGGCTCCACCAAGCAAGCACCACAGACCTTACGTGAACACC 127

QY 188 TCAACGCTGCGGAGAGGATCTCGGCCCTGTGGCAAGGAGGATGCTTACCAGG 247
DB 128 TCAACGCGCGGAGAGGCTGCTGAGGCGAGCGCGCGGAAAGAGTGTGTTAAGCAGA 187

QY 248 TTAAGCTTCAGTCTGCTCAAGTTCAAGGAGGAGGAGACATCAATCACTCTCTGTTCT 307
DB 188 TCCAGCTGCAAGTGGGATCAAGTTCAACGCGGTGGCCACATCAACACTCGTGTCT 247

QY 308 GGAAGAACTTGGCTCCCTATGAGATCCGAGAGGCTTACCTCTCTGAAGGACTCTCAAGA 367
DB 248 GGAAGAACTTGGCCCCCAGAGCGAGGCTGTGGCCAACTGAAGATGGCCCTCTCAAGC 307

QY 368 AGGCTATCGAGAACTCTTTTGGTTCTTTCGAGGCTTCAAGAGAAAGTTCAAGCTGACA 427
DB 308 AGGCCATCGAGCAGGAGTTCGGCGACTTTGAGAAAGTTCAAGACGACCTTCAACAGGAG 367

QY 428 CCGCTGCTGCCAAGGATCCGATGGGCTGGCTTGGCTTGAACCCGCTTACTTAGAAGC 487
DB 368 CGGCGGCGATCAGGCTTGGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 424

QY 488 TGAAGTCAACACGACCCCAACAGGACCTCTGCTTACTTACTTACTTACTTACTTACTTACT 547
DB 425 TCGACCTGGTCTGTTGCCAAGGCGCAGGACCCGCTCAAGCAGCACCACCCCGCTGCTGCT 484

QY 548 TTGACATCTGGGAGCAGCTTCTTACCTTCTAGTCAAGAAAGTCAAGCTGACTATCTCG 607
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QY 434 CTGTCAAGATCCGATCGGCTGGCTTGGCTTGAACCGCTTACTTAAGAAGCTCGAAG 493
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 Db 552 CGTGGAGACCGGTTCTTACCTGACGACCAAGCTCAAGGCGGCTACTTCAAGGCGCA 611
 QY 614 TTTGGTCCGTTTACTACGAGGAGCGAGCGGATTCAGGCTGCTCTC 666
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 LOCUS 812 bp mRNA linear PAT 26-SEP-2002
 DEFINITION Sequence 7 from patent US 6432407.
 ACCESSION AR222758
 VERSION AR222758.1 GI:23330440
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 812)
 AUTHORS Takesako, K., Okado, T., Yagihara, T., Kuroda, M., Onishi, Y., Kato, I., Akiyama, K., Yasueda, H. and Yamaguchi, H.
 TITLE Antigenic protein originating in malassezia
 JOURNAL Patent: US 6432407-A 7 13-AUG-2002;
 FEATURES Location/Qualifiers
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 Best Local Similarity 63.9%; Pred. No. 4.9e-56;
 Matches 379; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

 QY 74 CAAGCATACCTGCTGAGTTCCTTACGCTTACGATGCGCTGGAGCGCTCCATCTCCA 133
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 QY 194 CTGCCGAGGAGCTACTCGGCGCTGTGGCAAGGAGGATGTGCTTACCAGGTTAAGC 253
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 QY 254 TTGAGTCTGCTCAAGTTCAACGAGGAGAGACATCAATCACTCTCTGTTCTGGAGA 313
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QY 554 TCTGGAGACGCTTCTACCTTCACTACAGAACGCTCAAGCTCACTATCTCGCTGCTG 613
 Db 552 CGTGGAGACCGGTTCTTACCTTCACTGAGTACAGAACGCTCAGCGCTACTTCAAGGCGCA 611
 QY 614 TTTGGTCCGTTTACTACGAGGAGCGAGCGCGATTCAGGCTGCTCTC 666
 Db 612 TCTGGACCGTGATCAACTTTGAGGAGCGGAGAGCGTCTCAAGGAGGCGCTC 664

 RESULT 11
 AF114848
 LOCUS 621 bp mRNA linear PLN 16-APR-1999
 DEFINITION Paxillus involutus manganese-superoxide dismutase precursor (MnSOD)
 mRNA, complete cds.
 ACCESSION AF114848
 VERSION AF114848.1 GI:4585262
 KEYWORDS
 SOURCE Paxillus involutus
 ORGANISM Paxillus involutus
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Boletales; Paxillaceae; Paxillaceae; Paxillus.
 REFERENCE 1 (bases 1 to 621)
 AUTHORS Jacob, C., Courbot, M., Botton, B. and Chalot, M.
 TITLE Cloning and sequencing of a full-length cDNA encoding the manganese superoxide dismutase precursor of the ectomycorrhizal fungus, Paxillus involutus
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 621)
 AUTHORS Jacob, C., Courbot, M., Botton, B. and Chalot, M.
 TITLE Direct Submission
 JOURNAL Submitted (17-DEC-1998) Forest Biology, University H. Poincare, Vandoeuvre 54506, France
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 ORIGIN
 Query Match 36.9%; Score 246.6; DB 8; Length 621;
 Best Local Similarity 66.0%; Pred. No. 5.6e-55;
 Matches 398; Conservative 0; Mismatches 184; Indels 21; Gaps 2;

 QY 77 AGCATACCTCGCTGAGCTTCCTTACGTTACGATGCGCTGGAGCCCTCCATCTCCAGG 136
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 QY 137 AGATCATGACCTTCACACACCAACCAACCATCAGACTTATGTTAACGGCTCAACGCTG 196
 Db 71 AGATCATGACGCTTCACACCAAGAGGACCAACCAACCTATGCTCACTGCTCTCAACGCGC 130
 QY 197 CCGAGGAGAGCTACTCGGCCCTGTGGCAAGGAGGATGTCTTACCAGGCTTAAGCTTC 256
 Db 131 CTGAATCATGTTACCGAGAGACTCTACTCTCCAGAGGCGCATCGCC-----CTCC 181
 QY 257 AGTCTGCTCTCAAGTTCAACGGAGGAGGACATCAATCACTCTCTGTCTTGGAGAAGAT 316

3797253
 2 (bases 1 to 779)
 Sun, Y., Hegamyer, G. and Colburn, N.H.
 Sequence of manganese superoxide dismutase-encoding cDNAs from
 multiple mouse organs
 Genes 131 (2), 301-302 (1993)
 94010326
 PUBLISHED
 8406027
 PubMed
 Sun, Y.
 Direct Submission
 3 (bases 1 to 779)
 Submitted (25-NOV-1992) Sun Y., FCRDC, CBS, LVC, P.O. Box B,
 Frederick, MD, 21702-1201
 JOURNAL
 TITLE
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 69 CAGGCAAGCATACCTCGCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT 128
 101 CCGGCACAAGCACAGCCTCCAGACCTGCTTACGACTATGGCGGCTGGAGCCACAT 160
 129 CTCCAAGGAGATCATGACCTTCACCACCAAGCACCATCAGATTATGTTAAGCGCT 188
 161 TAACGCGCAGATCATGAGCTGCACCAAGCACCATGCGGCTACGTGAACACCT 220
 189 CAACGCTGCCGAGGAGACTACTCGGCGCTGTGGCAAGGAGATGTCTTACCAGGT 248
 221 CAACGCCACCGAGGAGATACCAAGGCTCTGCGCAAGGAGATGTCAACTCAGGT 280
 249 TAAGCTTCAGTCTGCTCTCAAGTTCACGAGGAGGACATCAATCACTCTCTGTCTG 308
 281 CGCTCTTCAGCCTGCACTGAAGTTCAATGTGGGGACATATTAATCACACCATTTCTG 340
 309 GAAGAACTTGCTCCCTATGATCGGAGGAGGTACCTCTCTGAGGACCTCTCAAGAA 368
 341 GACAACTGAGCCCTAAGGTGGTGGAGAACCTA-----AAGGAGATTGCTGGA 391
 369 GGCTATCGAGGAATCTTTTGGTCTTTTCGAGGCTTCAAGAGAGATTCAACGCTGACAC 428
 392 GGCTATCAAGCGTGACTTTGGTCTTTTGAAGATTTAAGGAGAGCTGACAGCCGTGTC 451

QY 429 CGCTGCTGTCCAAGGATCCGATCGGCTGGCTTGGCTTGAACCCGCTTACTAAGAAGCT 488
 Db 452 TGTGGAGTCCAAAGGTTTCAAGGCTGGGCTGGCTTGGCTTCAATAGGAGCAAGGTCGCTT 511
 QY 489 GGAAGTCAACACGACCGCCCAACACGAGACCTCTGC-----TTACTCACATTCTTAT 539
 Db 512 ACAGATTGCTGCTGCTCTAATCAGGACCCATTGCAAGGACAAACAGGCTTATTCGCT 571
 QY 540 CATCGAGTTGACATCTGGAGCAGCTTTCTACCTTCACTACAGTACAGAGCTCAAGCTGA 599
 Db 572 GCTGGGATTTGACGTTGGGAGCAGCTTACTACCTTCAGTATATAAAACGTCAGACCTGA 631
 QY 600 CTATCTCGCTGCTGTTTGGTCCGTTTATCAACTACAGGAGG 640
 Db 632 CTATCTGAAGCTATTGGAATGTAATCACTGGGAGAAATG 672

Search completed: April 1, 2004, 18:48:00
 Job time : 2590.54 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2004, 13:12:34 ; Search time 1718 Seconds

(without alignments)
11628.541 Million cell updates/sec

Title: US-09-727-855B-4

Perfect score: 669

Sequence: 1 atgtctgtctgagcatccct.....gattgcaggctgtctcttaa 669

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthm:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estom:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrt:*

28: gb_gssl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	285.8	42.7	754	14	CF638868
2	284.4	42.5	656	14	CF644174
3	284.4	42.5	662	14	CF643783
4	284.4	42.5	702	14	CF643817

5	267	39.9	617	14	CF643863	CF643863 K13_E08 F
6	260.4	38.9	776	14	CA765001	CA765001 AF53-RP
7	221.6	33.1	634	14	CD489102	CD489102 T18_F10 T
8	215.6	32.2	606	14	CD271903	CD271903 T143A0136
9	215.4	32.2	736	14	CF472965	CF472965 RTD5L12
10	212.4	31.7	619	14	CF643518	CF643518 D91_E07 F
11	212.2	31.7	730	12	BI904486	BI904486 603168211
12	211	31.5	995	14	CF583893	CF583893 AGENCOURT
13	210.8	31.5	746	13	BU060841	BU060841 Fgr-C 1 K
14	210.4	31.4	577	14	CD488011	CD488011 T03_D04 T
15	209.6	31.3	468	9	AT002967	AT002967 AT002967
16	209.6	31.3	539	14	CD272097	CD272097 T143A0126
17	208.2	31.1	719	12	BG970432	BG970432 602837995
18	208.2	31.1	748	14	CA321590	CA321590 UI-M-FXO-
19	208.2	31.1	825	12	BI412406	BI412406 602986655
20	208.2	31.1	828	14	CD467777	CD467777 LeukoS1.6
21	208.2	31.1	835	12	BI409485	BI409485 602961858
22	208.2	31.1	867	14	CB590330	CB590330 AGENCOURT
23	208.2	31.1	900	11	AK002428	AK002428 Mus muscu
24	208.2	31.1	909	12	BI415463	BI415463 602987460
25	208.2	31.1	914	11	AK012354	AK012354 Mus muscu
26	208.2	31.1	915	13	BY702957	BY702957 BY702957
27	208.2	31.1	1001	13	BY703048	BY703048 BY703048
28	208.2	31.1	1140	13	BU525570	BU525570 AGENCOURT
29	208.2	31.1	1171	11	AK002534	AK002534 Mus muscu
30	207.8	31.1	640	9	AU170704	AU170704 AU170704
31	207.8	31.1	643	9	AU169164	AU169164 AU169164
32	207.6	31.0	692	14	CB966783	CB966783 NL42_D11
33	207.6	31.0	721	13	BU673715	BU673715 NL19_29
34	207.2	31.0	538	14	CD270886	CD270886 T143A0140
35	207.2	31.0	890	13	BU505768	BU505768 AGENCOURT
36	206.6	30.9	739	14	CD298026	CD298026 AGENCOURT
37	206.6	30.9	830	14	CB668854	CB668854 OSJNEd160
38	206	30.8	793	14	CB627323	CB627323 OSJNEd160
39	206	30.8	807	14	CB627324	CB627324 OSJNEd160
40	206	30.8	826	14	CB668853	CB668853 OSJNEd160
41	206	30.8	841	14	CB668027	CB668027 OSJNEd15K
42	205.8	30.8	556	9	AW064502	AW064502 PicSSH13
43	204.6	30.6	755	14	CB668028	CB668028 OSJNEd15K
44	204.6	30.6	784	12	BI691345	BI691345 603309664
45	203.8	30.5	901	14	CD459143	CD459143 F908_05D0

ALIGNMENTS

RESULT 1	CF638868	754 bp	mrna	linear	EST 02-OCT-2003
LOCUS	D08_A03 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA				
DEFINITION	CF638868				
ACCESSION	CF638868				
VERSION	CF638868.1	GI:37402948			
KEYWORDS	EST.				
SOURCE	Ustilago maydis				
ORGANISM	Ustilago maydis				
REFERENCE	1 (bases 1 to 754)				
AUTHORS	Nugent, K.G., Choffe, K. and Saville, B.J.				
TITLE	Gene Expression during Ustilago maydis Diploid Filamentous Growth:				
JOURNAL	EST Library Creation and Analyses				
COMMENT	Unpublished (2003)				
	Contact: Barry J. Saville				
	Saville Lab				
	University of Toronto				
	3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada				
	Tel: 905 569 4702				
	Fax: 905 828 3792				
	Email: bsaville@utoronto.ca				
	Plate: UTM-UM-D126/7-008-UTM row: 03 column: A				
	Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')				
	High quality sequence stop: 754.				

QY 599 ACTATCTCGCTGCTGTTTGGTTCGGTATCACTAACAGGAGGAGGCGCCGCTTCAAGG 658
 |||||
 Db 585 ACTACTTCAAGAACATTGTGCTGCATCACTTCAAGGAGGCGGAGGCGCTTCAAGG 644
 |||||
 QY 659 CTGCTC 664
 |||||
 Db 645 CTGCCC 650

RESULT 3
 CF643783
 LOCUS
 DEFINITION
 K12_E10 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CF643783
 662 bp mRNA linear EST 02-OCT-2003
 K12_E10 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

CF643783
 1 GI:37412406

Ustilago maydis
 Ustilago maydis
 Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 1 (bases 1 to 662)
 Nugent, K.G., Choffe, K. and Saville, B.J.
 Gene Expression during Ustilago maydis Diploid Filamentous Growth:
 EST Library Creation and Analyses
 Unpublished (2003)
 Contact: Barry J. Saville
 Saville Lab
 University of Toronto
 3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
 Tel: 905 569 4702
 Fax: 905 828 3792
 Email: bsaville@utm.utoronto.ca
 Plate: UTM-UM-D128/9-012-UTM row: 10 column: E
 Seq primer: T7 Reverse (5' GAGTAATACGACTACTATAGG 3')
 High quality sequence stop: 662.

FEATURES
 source
 1..662
 /organism="Ustilago maydis"
 /mol_type="mRNA"
 /strain="FBD12"
 /db_xref="taxon:5270"
 /cell_type="Mycelia"
 /dev_stage="Filamentous diploid"
 /clone_lib="Filamentous Forced Diploid"
 /note="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN
 Query Match 42.5%; Score 284.4; DB 14; Length 662;
 Best Local Similarity 66.8%; Pred. No. 3.1e-66;
 Matches 405; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 59 CTTTCAGATCAGGCGAAGCATACCTCGCTGAGCTTCCTTACGCTTACGATGCCCTGG 118
 |||||
 Db 54 CTCTGCCCAAAATGTCGAGCACACCTTCCCGAGCTCCCTTACGCTACATGACTCG 113
 |||||
 QY 119 AGCCCTCCATCTCCAGGAGATCATGACCTTCACACACCAGACCATCATGACTATG 178
 |||||
 Db 114 AGCCCGCCATCTCGGAGGAGATCATGACCATCCACACCAAGACCACTGCTTAAG 173
 |||||
 QY 179 TTAAGCGCTCAACGCTGCGGAGGAGCTACTCGGCCCTGTGGCAAGGAGGATGTC 238
 |||||
 Db 174 TCACCATCTCAACACGCTATCAAGCCCTACACTCGGCCCATCTCGACACGAGCTTC 233
 |||||
 QY 239 TTAACGAGTTAAGTTCAAGTCTGCTCTCAAGTTCAACGGAGGAGGACATCAATCACT 298
 |||||
 Db 234 GCAAGCAGATTGAGTCCAGAGGCCATCAAGTTCAACGGCGGTGGCCACATTACCAT 293
 |||||
 QY 299 CTCTGTTCTGGAAGAACTTGGCTCCCTATGATTCGAGGAGGCTACCTCTCTGAAGGAC 358
 |||||

Db 294 CGCTCTTCTGGAAGAACCTTGTCTCTCCAGCGAGGCGGTGGACACGCTTCAAGATGGTC 353
 |||||
 QY 359 CTCTCAAGAGGCTATCGAGGAATCTTTTGGTTCCTTTTCGAGGCTTCAAGAGAGTTCA 418
 |||||
 Db 354 CTTTCAAGCAGGCGCTCGAAACGTCGCTTGGCTCGCTCGACAACTCAAAATCCACCTTCA 413
 |||||
 QY 419 ACCTGACACCGCTGCTGTCTCAAGGATCGGATGGGCTTGGCTTGAACCCGCTTA 478
 |||||
 Db 414 ACCTTACCATTGCCACCATCCAGGCTCTGGTGGGCTGGCTGGTTTCAACCCCAAGA 473
 |||||
 QY 479 CTAAGAAGTGGAGTCAACACGACCGCCAAACAGGACCCCTCTGCTTACTCACTTCTTA 538
 |||||
 Db 474 ACTCGAAGCTTGAAGTTGTCAACCAAGGACGAGACCCCTCTGATCTCGCACCCCA 533
 |||||
 QY 539 TCATCGGAGTTGACATCTGGGAGCAGCTTTTACCTTCACTCAAGAGAGCTCAAGCTG 598
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 Db 534 TCATCGGAGTTCGACGCTTGGGAGCAGCTTTTACCTTCAAGAGAGCTCAAGCTG 593
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 QY 599 ACTATCTCGCTGCTGTTTGGTTCGGTTCATCAAGGAGGAGGCGCCGCTTGAAG 658
 |||||
 Db 594 ACTACTTCAAGACATTTGGTTCGCTCATCACTTCAAGGAGGCGGAGGCGCTTCAAG 653
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659 CTGCTC 664
 |||||
 Db 654 CTGCCC 659

RESULT 4
 CF643817
 LOCUS
 DEFINITION
 K13_A05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CF643817
 702 bp mRNA linear EST 02-OCT-2003
 K13_A05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

CF643817
 1 GI:37412471

Ustilago maydis
 Ustilago maydis
 Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 1 (bases 1 to 702)
 Nugent, K.G., Choffe, K. and Saville, B.J.
 Gene Expression during Ustilago maydis Diploid Filamentous Growth:
 EST Library Creation and Analyses
 Unpublished (2003)
 Contact: Barry J. Saville
 Saville Lab
 University of Toronto
 3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
 Tel: 905 569 4702
 Fax: 905 828 3792
 Email: bsaville@utm.utoronto.ca
 Plate: UTM-UM-D128/9-013-UTM row: 05 column: A
 Seq primer: T7 Reverse (5' GAGTAATACGACTACTATAGG 3')
 High quality sequence stop: 702.

FEATURES
 Location/Qualifiers
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 /organism="Ustilago maydis"
 /mol_type="mRNA"
 /strain="FBD12"
 /db_xref="taxon:5270"
 /cell_type="Mycelia"
 /dev_stage="Filamentous diploid"
 /clone_lib="Filamentous Forced Diploid"
 /note="Vector: pSport; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN
 Query Match 42.5%; Score 284.4; DB 14; Length 702;
 Best Local Similarity 66.8%; Pred. No. 3.3e-66;
 Matches 405; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

Ehrhartoidae; Oryzae; Oryza.
 1 (bases 1 to 776)
 Bennett, J., Arumugam, K., Lafitte, R., Wen, J., Rudd, S. and
 Bruskiewicz, R.M.
 TITLE
 IIRI Drought Stress Panicle cDNA Library
 JOURNAL
 Unpublished (2002)
 COMMENT
 On Dec 2, 2002 this sequence version replaced gi:25994256.
 Contact: Richard Bruskiewicz
 Biometrics and Bioinformatics Unit
 International Rice Research Institute
 DAPO 7777, Metro Manila, Philippines
 Tel: +63-2-845-0563
 Fax: +63-2-845-0606
 Email: r.bruskiewicz@cgiar.org
 International Rice Information System (IRIS;
 http://www.iris.irri.org): D0201832
 Assignment of putative function to the sequence by S. Rudd of the
 Munich Information Center for Protein Sequences
 (http://mips.gsf.de)
 Plate: 05 row: M column: 09.
 FEATURES
 source
 1..776
 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="IR64"
 /db_xref="taxon:39946"
 /clone="C0001833"
 /tissue_type="Panicles"
 /dev_stage="Flowering"
 /clone_lib="IRRI Drought Stress Panicle Library"
 /note="Vector: plasmid II SK+; Water stress was
 applied by not watering for 4 consecutive days. Panicles
 were collected from control (well watered) and stressed
 plants at 2 days before heading, at heading, 50% flowering
 and 4 days after 50% flowering."

ORIGIN

Query Match 38.9%; Score 260.4; DB 14; Length 776;
 Best Local Similarity 65.1%; Pred. No. 1.2e-59;
 Matches 385; Conservative 0; Mismatches 203; Indels 3; Gaps 1;
 QY 71 GGGCAAGCATACCTCGCTGAGTTCCTTACGTTACGATGCGCTCGAGCCCTCCACTCT 130
 Db 162 GCGGACAGCACACCTCGCTGAGTTCCTCGTAGGCTATGATGCGCTCGAGCGGCTCATCT 221
 QY 131 CCAAGGAGATCATACCTTCACACACCAAGGACCATGACATATGTTAAAGGCTCA 190
 Db 222 NGAAGGAGATCATGACGCTCCACACACCAAGGACCAAGGACCATGACATGAGGCTCA 281
 QY 191 ACGTGGCGGAGGAGTACTCGGCGCTGFGGCAAGGAGGATGCTTACCCAGGTTA 250
 Db 282 ATGCGCGGAGAGAGAGCGCGCCAGTTTCAACAGTCGGGCGAGCTCAAGGCGGAGATCA 341
 QY 251 AGCTTACGTTGCTCTCAAGTTCAACGAGGAGGACATCAATPACTCTCTGTCTGGA 310
 Db 342 ATTTCAGGCGCGCTTGAAGTTTAAAGGCTGAGGCTGACCTTGAACCACTCGCTCTTCTGGC 401
 QY 311 AGAATTTGGCTCCCTATGATTCGAGGAGGCTACCTCTCTGAAGGAC---CTCTCAAGA 367
 Db 402 GCAACCTCGGCGGACCGGACTCGGCGCTTACCAAGCGCGAAGCGGCTCCGACCTTTATCA 461
 QY 368 AGGCTATCGAGGAATCTTTTGTCTTTTCGAGGCTTTCAGAGAAAGTTCAACGCTGACA 427
 Db 462 AGCAGTTCGAAGGACTTTTGGATCCCTCGAGGCGCTCAAGATGAATCAACACCAAGA 521
 QY 428 CCGTGTCTGTCCAGGATTCGAGTGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAAGC 487
 Db 522 CGGCGCGATCCAGGATTCGAGTGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAAGC 581
 QY 488 TGAAGTCAACGACCGGCAACGAGGACCTCTGTCTTACTTCAATTCCTTATCATCGGAG 547
 Db 582 TGGACGTGGTCTACTTACTGCAACGAGGACCGCTTGGTGAAGTCTACGAGGCAATCTCTGCTA 641

QY 548 TTGACATCTGGAGCAGCTTCTTACCTTCAGTACAAAGACGTCAGCTCACTATCTCG 607
 Db 642 TCGACATCTGNAACACGCTTCTTACCTTCAGTACAAAGATGTCAGCTCACTATCTCA 701
 QY 608 CTGCTGTTTGGTCCGTTATCAACTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 658
 Db 702 AGGCACTGGAACGTTATCACTTTCGAAANATCGAAGAGCGCTTTTAAAG 752
 RESULT 7
 CD489102 634 bp mRNA linear EST 29-AUG-2003
 LOCUS
 DEFINITION
 T18 F10 Teliospore Ustilago maydis cDNA 5', mRNA sequence.
 ACCESSION
 CD489102
 VERSION
 CD489102.1 GI:34331609
 KEYWORDS
 EST.
 SOURCE
 Ustilago maydis
 ORGANISM
 Ustilago maydis
 Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 1 (bases 1 to 634)
 Sacadura, N.T. and Saville, B.J.
 Gene expression and EST analyses of Ustilago maydis germinating
 teliospores
 Fungal Genet. Biol. 40 (1), 47-64 (2003)
 MEDLINE
 22829673
 PUBMED
 12948513
 COMMENT
 Contact: Barry J. Saville
 Saville Lab
 University of Toronto
 3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
 Tel: 905 569 4702
 Fax: 905 828 3792
 Email: bsaville@utoronto.ca
 Seq primer: M13 reverse primer (5' AACACGCTATGACCATGTTC 3').
 FEATURES
 source
 1..634
 /organism="Ustilago maydis"
 /mol_type="mRNA"
 /strain="PBI/PB2"
 /db_xref="taxon:5270"
 /cell_type="Teliospore"
 /dev_stage="Germinating teliospore"
 /lab_host="E. coli"
 /clone_lib="Teliospore"
 /note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;
 mRNA was extracted from germinating teliospores. cDNA was
 amplified by PCR and unidirectionally cloned into pDNR-LIB
 plasmid, with the use of Clontech's Creator SMART cDNA
 Library Construction Kit."

ORIGIN

Query Match 33.1%; Score 221.6; DB 14; Length 634;
 Best Local Similarity 65.0%; Pred. No. 3.9e-49;
 Matches 357; Conservative 0; Mismatches 190; Indels 2; Gaps 2;
 QY 28 GTGCTTAGACAGACTTTCGTCGCTTCGCTGCTTTCAGATCAGGCAAGGACATACCTG 87
 Db 78 GCSTGCTGCGGAGTTTGTGCGCTCTGCGCCCTGCGGCGGAGCAAGCACACGCTT 137
 QY 88 CTTGAGCTTCTTACGCTTACGATGCGCTCGAGCCCTCCATCTCCAAGGAGATCATGACC 147
 Db 138 CCGACCTGCTTTCGACTACGCTGACTCGAGCCCGCAATTCATCCAAGATCATGGAG 197
 QY 148 CTTTACCACCAAGCACCACATCAGCTTATGTTAAAGGCGCTCAACGCTCGCGGAGGAGC 207
 Db 198 CTACCCACCAAGCACCACCAAGCCTATGTCACCGTCTCAACCGGCGGAGAGCAG 257
 QY 208 TACTCGGCCCTGTGGCAAGGAGATGCTCTTACCCAGGTTAAGCTTACGTTCTGCTCTC 267
 Db 258 CTCTCTGAAGCGATCCACAAAGAGGAGCTCAAGTCGGCAATCGCTCTTCAGAAAGCGATC 317
 QY 268 AAGTTCAACGAGGAGGAGACATCACTCTCTGTCTTGGAAAGACTTGGCTCCCTAT 327

QY 367 AAGGCTATCGAGAAATCTTTTGGTTCTTTCGAGGCTTCAAGAAGAGTTCAACGCTGAC 426
 |||||
 Db 199 CAGGCGTGAAGCTGACCTTGGCTCGCTCGACAACTCAATCCACCTTCAACGCTACC 258
 |||||
 QY 427 ACGCTGCTGTCAAGATCCGATGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAAG 486
 |||||
 Db 259 ATTGCCACCATCCAGGCTCTGGTTGGGCTGGCTCGTTTCAACCCCAAGAACTCGAAG 318
 |||||
 QY 487 CTGGAAGTCACACGACCGCCACACGAGGACCTCTGCTTACTACATCTCTATCATCGGA 546
 |||||
 Db 319 CTTGAGTTGTACCAACCAAGGACCAAGGACCTCTGATCTCGACCAACCCCATCATCGGT 378
 |||||
 QY 547 GTTGACATCTGGAGACGCTTTTCTACTCTTCACTACAAGAACTCAAGCTGCTGACTATCTC 606
 |||||
 Db 379 GTGACGCTGGGAGCAGCGTTTCTACTCTCCAGTACAGAAGTGTAAAGGCTGACTACTTC 438
 |||||
 QY 607 GCTGCTGTTTGGTCCGTTATCAACTACAAGGAGGAGAGGCGGATGAGGCTGCTC 664
 |||||
 Db 439 AAGAACATTTGGTCGCTATCACTTCAAGGAGGCGGAGGCGCTTCAAGGCTGCC 496
 |||||

RESULT 11

BI904486 730 bp mRNA linear EST 16-OCT-2001
 603168211F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5256195 5',
 mRNA sequence.

BI904486
 BI904486.1 GI:16166831

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 730)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAW1847 row: f column: 04

High quality sequence stop: 724.

Location/Qualifiers

1..730

/organism="Mus musculus"

/mol_type="mRNA"

/strain="Czech II"

/db_xref="taxon:10090"

/clone="IMAGE:5256195"

/tissue type="pooled lung tumors"

/lab_host="PH108 (phage-resistant)"

/clone_lib="NCI_CGAP_Lu33"

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st

strand cDNA was prepared from mRNA obtained from pooled

lung tumors with a Not I - oligo(dT) primer [5',

TGTTACCAATCTGAAGTGGAGCGCGCTGTTTATTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not

I and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match

31.7%; Score 212.2; DB 12; Length 730;

Best Local Similarity 63.4%; Pred. No. 1.5e-46;
 Matches 366; Conservative 0; Mismatches 193; Indels 18; Gaps 2;

QY 69 CAGGGCAAGACATACCTGCTGAGCTTCCTTACGCTTACGATGCCCTGAGCCCTCCAT 128
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 Db 159 CCGGCAAGACACAGCTCCAGACCTGCTTACGACTATGGCGCTGAGCCACACAT 218
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 QY 129 CTCRAAGGAGATCATGACCTTACCACACCAAGACCATCAGACTATGTTAAACGCT 168
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 Db 219 TAAAGGCGAGATCATGACCTGACCAACAGCAAGACCATGCGCTTACGTAACACCT 278
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 QY 189 CAACGCTGCCGAGGAGAGCTACTCGGCCGCTGTGGCAAGAGGAGTGTGTTACCCAGGT 248
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 Db 279 CAACGCCACCGAGGAGAGTACCAGAGGCTCTGGCCAAAGGAGATGTTACAACTCAGGT 338
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 QY 309 GAAGAACTTGGCTCCCTATGATCGAGGAGGCTACCTCTCTGAAGGACCTCTCAAGAA 368
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 QY 540 CATCGAGTTGACATCTGGAGCAGCGCTTCTACCTTCAGTACAGAACGCTCAAGCCTGA 599
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 Db 630 GCTGGGATTGACGTTGGGAGCAGCGCTTACTACCTTCAAGTATAAAAGCTCAGACCTGA 689
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 QY 600 CTATCTCGCTGCTGTTTGGTCCGTTATCAACTACAG 636
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 Db 690 CTATCTGAAAGCTATTGGAATGTAATCAACTGGGAG 726
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RESULT 12

CF583893

LOCUS

DEFINITION

AGENCY: 11364483 updated NIH MGC_137 Mus musculus cDNA clone

IMAGE: 6431706 5', mRNA sequence.

CF583893

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 995)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NTH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)

cDNA Library Preparation: Catherine Lee, Endocrine Pancreas

Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: IRBD19 row: b column: 07
 High quality sequence start: 21
 High quality sequence stop: 522.
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 /note="Organ: pancreas; Vector: pSPORT1; Site 1: SalI; Site 2: NotI; library consists of a pool of clones rearrayed from the following libraries: Melton normalized mixed mouse pancreas 1 NI-MMS1, Amplified Melton mouse islets 1 MSL1-A, and Kaestner ngm3 wt. Clones rearrayed in the laboratory of K. Kaestner (University of Pennsylvania). Note: this is a NIH_MGC Library."
 source

ORIGIN

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 Best Local Similarity 63.2%; Pred. No. 3.9e-46;
 Matches 366; Conservative 0; Mismatches 195; Indels 18; Gaps 2;
 QY 69 CAGGGCAAGCATACCTGCTGAGTTCCTTACGCTTACGCTTACGCTGAGCCCTCCAT 128
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 Db 184 TAAGCGCAGATCATGCGCTGACGACACACAGCACCATGCGGCTACGTGAACACCT 243
 QY 189 CAACGCTGCCGAGAGAGTACTCGGCGCTGTGGGCAAGGAGATGTCTTACCAGGT 248
 Db 244 CAACGCCACCGAGAGAGTACCAAGGCTCTGGCAAGGAGATTTACAACCTCAGGT 303
 QY 249 TAAGCTTCAGTGTCTCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTCTG 308
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 QY 309 GAAGAACTTGGCTCCCTATGATCCGAGGAGGTACCTCTCTGAAGACCTCTCAAGAA 368
 Db 364 GACAACTGAGCCCTAAGGCTGTGGAGAACCA-----AAGGAGATGCTGGA 414
 QY 369 GGCTATCGAGGAATCTTTGGTCTTTTCGAGGCTTCAAGAGAGTTCAAGCTGACAC 428
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 QY 429 CGCTGTCTCCAGGATCCGATGGGCTGGCTTGGCTTGAACCGCTTACTAAGAGCT 488
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 QY 489 GGAAGTCACCAAGCCGCAACAGGACCTCTGCTC-----TTACTCACATTCCTAT 539
 Db 535 ACAGATTGCTGCTGCTTAATCAGGACCCATTCGAAGGACACAGGCTTATTCGCT 594
 QY 540 CATCGGATTTGAATCTGGGAGACGCTTCTTACCTTCAGTACAGAGCTCAAGCTGA 599
 Db 595 GCTGGGATTTGACGTGTGGGAGCAGCTTACTACCTTCAGTATATAAAGCTGACACCTGA 654
 QY 600 CTATCTCGTGTCTTTGGTCCGTTATCACTACAAGGA 638
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RESULT 13
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 DEFINITION 746 bp mRNA linear EST 26-AUG-2002
 sequence.
 BU060841
 ACCESSION BU060841.1 GI:22501130
 VERSION
 KEYWORDS EST.

Gibberella zeae
 Gibberella zeae
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 1 (bases 1 to 746)
 Trail, F., Xu, J.-R., San Miguel, P., Haigren, R.G. and Kistler, H.C.
 Analysis of expressed sequence tags from Gibberella zeae (anamorph
 Fusarium graminearum)
 Fungal Genet. Biol. 38 (2), 187-197 (2003)
 22508120
 12620255
 Contact: Frances Trail
 Department of Plant Biology
 Michigan State University
 East Lansing, MI 48824, USA
 Tel: 517 432 2939
 Fax: 517 353 1926
 Email: trail@msu.edu
 Plate: 1 row: K column: 18.
 Location/Qualifiers
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 Best Local Similarity 61.9%; Pred. No. 3.7e-46;
 Matches 351; Conservative 0; Mismatches 213; Indels 3; Gaps 1;
 QY 68 TCAGGGCAAGCATACCTGCTGAGTTCCTTACGCTTACGCTGAGCCCTCCCA 127
 Db 126 TCCGCGGCAAGGCATCTCCCGATCTTCCCTTACGCTATGGCGCTTTGAGCCCTACA 185
 QY 128 TCTCCAAGGAGATCATGACCTTCAACACCAAGCACCATCAGACTTATGTTAAGGCC 187
 Db 186 TCTTGCCGAGATCTGGAGCTTCAACATCCCAAGCACCAGACTAGTTACCGCT 245
 QY 188 TCAACGCTGCCGAGGAGAGTACTCGGCCGCTGTGGCAAGGAGGATGTCTTACCCAGG 247
 Db 246 TCAACAGCTTACCGAGCCATCGCGAGCCAAACACAGGCGCAGCCCAAGGCTGCTG 305
 QY 248 TTAAGCTTCACTGTCTCAAGTTCAAGGAGGAGACATCAATCACTCTGTGTTCT 307
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 Db 426 CTTCCATCAACGAGGACTTTTGGCTCTTTCAGGCGCTTCAAGAGGAGCAGCAACGCTACCC 485
 QY 428 CGGCTGTCTCAAGGATCCGATGGGCTGGCTTGGCTTGAACCCGCTTACTAAGAGC 487
 Db 486 TCGCGGATTCACAGGCTCGGCTGGGCTGGCTTGGCTTCAAGGAGCAGAAAGCTGGGACT 545
 QY 488 TGGAGTCAACAGCAGCCCAACAGGACCTCTGTCTTACTCAATTT---CCTATCATCG 544
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 Db 606 GCATTGAGCGCTGNGAGCAGCGCTTACTTACCTTCAGTACCAAGACCGCAAGGCGGAGTACT 665
 QY 605 TCGCTGCTGTTGGTCCGTTATCACT 631
 Db 666 TCAGCGCATCTGGGAGCTCATCACT 692

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RESULT 14
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VERSION       CD488011.1  GI:34330509
KEYWORDS      EST.
SOURCE        Ustilago maydis
ORGANISM      Ustilago maydis
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               Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE     1 (bases 1 to 577)
AUTHORS       Sacadura,N.T. and Saville,B.J.
TITLE         Gene expression and EST analyses of Ustilago maydis germinating
               teliospores
JOURNAL       Fungal Genet. Biol. 40 (1), 47-64 (2003)
MEDLINE       22829673
PUBMED        12948513
COMMENT       Contact: Barry J. Saville
               Saville Lab
               University of Toronto
               3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
               Tel: 905 569 4702
               Fax: 905 828 3792
               Email: bsaville@utoronto.ca
               Seq primer: M13 reverse primer (5' AAACAGCTATGACCATGTTCA 3').
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ORIGIN
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Matches 324; Conservative 0; Mismatches 173; Indels 1; Gaps 1;

QY 28 GTGCTAGACAGACTTTCGTCGCTCCTGCTGCTTTCCAGATCAGGCGAAAGCATCCCTG 87
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QY 88 CTTGAGCTTCTTAGCTTAGATGCTGCTGAGCCCTGAGCCCTCATCTCCAGGAGATCATGACC 147
DB 138 CCCGACCTGGCTTTGAGTACGGTGCACTCGAGCCCGCCATTTCATCAAGATCATGGAG 197

QY 148 CTTACACACCAAGCAGCATCAGACTTATGTTAAAGCCCTCAAGCTGCGGAGGAGAGC 207
DB 198 CTACACACACCAAGCATCAGACCTATGTCAACGCTCTCAACCGCGCGAGAGAGCAG 257

QY 208 TACTCGGCGGTGGGCAAGGAGATGTGCTTACCCAGGTTAAGCTTCAGTCTGCTCTC 267
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QY 268 AAGTTTCAAGGAGGAGACATCAATCAGTCTCTGTTCTGGAAGAACTTCGCTCCCTAT 327
DB 318 AACTTTAAGCGGTGGTGCATCAATCAACAGCTCTCTTTGGGAGATCTGCGCCCGAG 377

QY 328 GGATCCGAGGAGGTACCTCTCTGAAGGACCTCTCAAGAGGCTTATCGAGGAATCTTTT 387
DB 378 AAGAATGCGGTGGTGGAGTTGAGCAGCGGCGCTCTCAAGGAGCGCTATCGACCGAGACTTT 437

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DB 498 NGTTTGGGNTGGCTCGGCTACACCCGAGACCAAGAGCTCGACATNGTCACTACCGC 557
QY 507 CAACGAGGACCCCTCTGCT 524
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DEFINITION    AT002967 POSIM01 Pleurotus ostreatus cDNA clone 460LM, mRNA
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ACCESSION     AT002967
VERSION       AT002967.1  GI:6934694
KEYWORDS      EST.
SOURCE        Pleurotus ostreatus (oyster mushroom)
ORGANISM      Pleurotus ostreatus
               Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
               Agaricales; Pleurotaceae; Pleurotus.
REFERENCE     1 (bases 1 to 468)
AUTHORS       Lee,S.H., Kim,B.G., Kim,K.J., Lee,J.S., Yun,D.W., Hahn,J.H.,
               Kim,G.H., Lee,K.H., Suh,D.S., Kwon,S.T., Lee,C.S. and Yoo,Y.B.
               Comparative Analysis of Sequences Expressed during the
               Liquid-Cultured Mycelia and Fruit Body Stages of Pleurotus
               ostreatus
JOURNAL       Fungal Genet. Biol. 35 (2), 115-134 (2002)
MEDLINE       21838665
PUBMED        11848675
COMMENT       Contact: Kim BG
               Division of applied microbiology
               National Institute of Agricultural Science and Technology (NIAT)
               Seodundong, Suwon, Kyung-gi 441-707, South Korea
               Email: bgkim@niat.go.kr
               Submitted through BRIC(Biological Research Information Center) of
               Korea
               URL: http://bric.postech.ac.kr/.
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QY 336 GGAGCTTACCTCTCTGAAGGACCTCTCAAGAGCTATCGAGGAATCTTTTGGTTCTTT 395
DB 61 CGGAGGCAAACTTCAGATGGCCCTTGAAGCAAGCCATCGAAGAGACTTTGCAACCGT 120

QY 396 CGAGGCTTCAAGAAGAGTTCAACGCTGACACCGCTGCTGTCGAAGGATCCGATGGG 455
DB 121 CGAAGATTTCAAGAAAAGTTCAACACCAACCATGCTG-TGTCCAAGCGATGCTGGG 179

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QY 456 CTGGCTTGGCTTGAAACCGCTTACTAAGAAGCTGGAAGTCACACAGACCGCCACCAACAGGA 515
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QY 180 CTGGCTTGGATTCAATCCACCAAGAGAGCTCGAGTCAACAGACCGCCACCAACAGGA 239
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 300 CCAATACAGAAGCTGAAGCTGATTACCTCAATGCTATCTGGAACGTTATCAACTTCAA 359
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QY 636 GGAGGCGAGGCGCCGATTGCGAGGCTGCT 663
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-727-855B-4

Perfect score: 669

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Gapop 10.0 , Gapext 1.0

Searched: 2465228 seqs, 1869859620 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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3	252	37.7	728	US-10-109-670-3	Sequence 3, Appli
4	250.6	37.5	812	US-10-109-670-4	Sequence 4, Appli
5	220.6	33.0	630	US-10-109-670-29	Sequence 29, Appli
6	205	30.6	1492	US-09-917-800A-1627	Sequence 1627, Ap
7	202.8	30.3	987	US-10-424-599-90405	Sequence 90405, A
8	199.6	29.8	2217	US-10-424-599-90403	Sequence 90403, A
9	197.8	29.6	972	US-10-044-090-836	Sequence 836, App
10	197.8	29.6	996	US-10-198-846-13503	Sequence 13503, A
11	197.8	29.6	1026	US-09-954-456-1822	Sequence 1822, Ap
12	197.8	29.6	1026	US-10-342-887-509	Sequence 509, App
13	197.8	29.6	1026	US-10-342-887-1905	Sequence 1905, Ap
14	197.8	29.6	2825	US-10-198-846-13787	Sequence 13787, A
15	188	28.1	817	US-09-770-445-745	Sequence 745, App

16	185.4	27.7	894	14	US-10-247-671-122	Sequence 122, App
17	184.6	27.6	1067	10	US-09-971-429B-22	Sequence 22, Appli
18	182.2	27.2	1295	15	US-10-310-154-294	Sequence 294, App
19	178	26.6	2208	13	US-10-044-090-709	Sequence 709, App
20	170.8	25.5	732	14	US-10-230-331-9	Sequence 9, Appli
21	151.4	22.6	3632	9	US-09-727-855B-1	Sequence 1, Appli
22	142	21.2	371	14	US-10-109-670-25	Sequence 25, Appli
23	139	20.8	1143	9	US-09-818-564-1	Sequence 1, Appli
24	136	20.3	477	10	US-09-911-904-182	Sequence 182, App
25	134.6	20.1	1230025	15	US-10-289-762-1	Sequence 3227, Appli
26	133.4	19.9	600	9	US-09-738-626-3227	Sequence 1, Appli
27	133.4	19.9	3309400	9	US-09-738-626-1	Sequence 5397, Ap
28	127	19.0	639	14	US-10-156-761-5397	Sequence 1, Appli
29	127	19.0	9025608	14	US-10-156-761-1	Sequence 14744, A
30	123.4	18.4	424	9	US-09-960-352-14744	Sequence 16177, A
31	116	17.3	477	10	US-09-918-995-16177	Sequence 8, Appli
32	111.4	16.7	721	9	US-09-987-190-8	Sequence 11, Appli
33	111	16.6	344	10	US-09-918-995-24298	Sequence 4975, Ap
34	107	16.0	325	9	US-09-993-333-11	Sequence 13978, A
35	106	15.8	419	9	US-09-960-352-4975	Sequence 731, App
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39	100.4	15.0	398	9	US-09-960-352-14457	Sequence 5493, Ap
40	98.6	14.7	456	9	US-09-960-352-12575	Sequence 67, Appli
41	98	14.6	425	9	US-09-960-352-5493	Sequence 45520, A
42	93.8	14.0	376	9	US-09-920-455-67	Sequence 5724, Ap
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ALIGNMENTS

RESULT 1

US-09-727-855B-4

; Sequence 4, Application US/09727855B

; Patent No. US20020168703A1

; GENERAL INFORMATION:

; APPLICANT: HOSHINO, Tatsuo

; APPLICANT: OJIMA, Kazuyuki

; APPLICANT: SETOGUCHI, Yutaka

; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL

; TITLE OF INVENTION: MATERIALS THEREOF

; FILE REFERENCE: C38435/111694

; CURRENT APPLICATION NUMBER: US/09/727,855B

; CURRENT FILING DATE: 2000-12-01

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 669

; TYPE: DNA

; ORGANISM: Phaffia rhodozyma

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(666)

; OTHER INFORMATION: n or x = A, C, G or T

US-09-727-855B-4

Query Match 100.0%; Score 669; DB 9; Length 669;

Best Local Similarity 100.0%; Pred. No. 2.6e-213; Indels 0; Gaps 0;

Matches 669; Conservative 0; Mismatches 0;

Qy	1	ATGTCGTTCGAGCATCCCTCTCTTCGTCGTCTAGACAGACTTTCGTCGCTCTCGTCTGCT	60
Db	1	ATGTCGTTCGAGCATCCCTCTCTTCGTCGTCTAGACAGACTTTCGTCGCTCTCGTCTGCT	60
Qy	61	TTCCAGATCAGGCGAAGCATACCTGCTGAGCTTCCTTACGCTTACGAGCCCTGGAG	120
Db	61	TTCCAGATCAGGCGAAGCATACCTGCTGAGCTTCCTTACGCTTACGAGCCCTGGAG	120
Qy	121	CCCTCCATCTCCAGGAGGATCATGCCCTTCACCAACCAACCATCAGACTTATGTT	180

QY 248 TTAGCTTCAAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCACTCTCTGTCT 307
 Db 188 TCCAGCTGCGAGATGCGATCAAGTTCAACGGGTGGCCACATCAACCATTCGCTGTCT 247
 QY 308 GGAAGACTTGGCTCCCTATGATCCGAGGAGGTACCTCTCTGAAAGGACCTCTCAAGA 367
 Db 248 GGAAGACCTGGCCCCCAGAGGAGGAGGTGGTGGCCAACTGAACGATGGCCCTCTCAAGC 307
 QY 368 AGGATATCGAGGATCTTTTGGTTCTTTTCAGGCTTCAAGAGAGATTCAACGCTGACA 427
 Db 308 AGGCCATCGAGCAGGAGTTTCCGCGACTTTTGAAGATTCAAGACGACCTTCAACACGAGG 367
 QY 428 CCGCTGCTGCCAAGGATCCGATGGGCTTGGCTTGGCTTGAACCCGCTTACTAAGAAC 487
 Db 368 CGGCGGATCCAGGTTTGGCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 424
 QY 488 TGAAGTCAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 547
 Db 425 TCGACCTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 484
 QY 548 TTGACATCTGGGAGCAGCTTTTACCTTCACTACAGAGAGGAGGAGGAGGAGGAGGAGGAGG 607
 Db 485 GGGATGCTGGGAGCAGCGCTTACCTGAGTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 544
 QY 608 CTGCTGTTGGTCCGTTTATCAACTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 655
 Db 545 AGGCTGGTGAAGCTGGTGAAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 592

RESULT 4
 US-10-109-670-4
 ; Sequence 4, Application US/10109670
 ; Publication No. US20030105283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TAKESAKO, KAZUTOH et al.
 ; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
 ; FILE REFERENCE: 1422-0523P
 ; CURRENT APPLICATION NUMBER: US/10/109,670
 ; CURRENT FILING DATE: 2002-04-01
 ; NUMBER OF SEQ ID NOS: 58
 ; SEQ ID NO 4
 ; LENGTH: 812
 ; TYPE: DNA
 ; ORGANISM: Malassezia furfur
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(812)
 ; OTHER INFORMATION: Strandedness:double-Topology:linear-Molecule Type:cDNA to mRNA
 US-10-109-670-4

Query Match 37.5%; Score 250.6; DB 14; Length 812;
 Best Local Similarity 63.9%; Pred. No. 3.6e-73;
 Matches 379; Conservative 0; Mismatches 214; Indels 0; Gaps 0;
 QY 74 CAAAGCATACCTGCTGCTGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTT 133
 Db 72 CCAAGTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 131
 QY 134 AGGAGATCATGACCTTCCACACACCAAGCACCACCTACGACTTATGTTTAAAGGCTCAACG 193
 Db 132 GCGAGATCATGAGACGCACTTACGAGAAGCACCACCGCACCTACGTCACAAACCTGAACG 191
 QY 194 CTGCGGAGGAGAGTACTCGGCGCTGCTGGCAGAGGAGTGTCTTACCCAGGTTAAGC 253
 Db 192 CCGCGGAGGAGCAAGCTGATGACGCGCTCCGCGAGCAGAGCCGCTCGGCGAGATTGCGC 251
 QY 254 TTGAGTCTGCTCAAGTTCAACGAGGAGGAGCAGACATCACTCTCTGTTCTTGGAGA 313
 Db 252 AGCTGAACGAGATCAAGTTCAACGCGGTGGCCACATCAACCATCTGCTCTTCTGGAGA 311
 QY 314 ACTTGGCTCCCTATGATTCGAGGAGGAGTACCTCTCTGAGGAGCTTCTCAAGAAGGCTA 373

Db 312 ACCTCGCGCCGACGAAACAAGGGCGGGCGAGCTCGACTCGGGCGAGCTGGCTCGCGCA 371
 QY 374 TCGAGGATCTTTTGGTTCTTTTCAGGCTTCAAGAGAGTTTCAACGCTGACACCGCTG 433
 Db 372 TCGACCGCGACTTTGGCTCGGTGAGCCCATGAAGGAGAGTTTCAACGCGCGCTCGCGG 431
 QY 434 CTGTCCAAGGATCCGATGGGCTTGGCTTGGCTTGAACCCGCTTACTTAAAGAGCTGGAAG 493
 Db 432 GCATCCAGGCGAGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 491
 QY 494 TCACACGACCGCAACACGAGCCCTCTGTTACTTCACTTCACTTCACTTCACTTCACTTCACTT 553
 Db 492 TCATACGACCGCAACACGAGCCGCTCTGCTGCGACAAGCCGCTGATTGGCATCGATG 551
 QY 554 TCTGGGAGCAGCTTCTTACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 613
 Db 552 CGTGGGAGCAGGCTTCTTACCTGAGTACAGAACGTCAGAGCGGCTCAAGGCGGCTTCAAGGCGCA 611
 QY 614 TTTGGTCCGTTATCAACTACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 666
 Db 612 TCTGGACCGTGATCAACTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 664

RESULT 5
 US-10-109-670-29
 ; Sequence 29, Application US/10109670
 ; Publication No. US20030105283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TAKESAKO, KAZUTOH et al.
 ; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
 ; FILE REFERENCE: 1422-0523P
 ; CURRENT APPLICATION NUMBER: US/10/109,670
 ; CURRENT FILING DATE: 2002-04-01
 ; NUMBER OF SEQ ID NOS: 58
 ; SEQ ID NO 29
 ; LENGTH: 630
 ; TYPE: DNA
 ; ORGANISM: Malassezia furfur
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(630)
 ; OTHER INFORMATION: Strandedness:double-Topology:linear-Molecule Type:cDNA to mRNA
 US-10-109-670-29

Query Match 33.0%; Score 220.6; DB 14; Length 630;
 Best Local Similarity 62.5%; Pred. No. 3.7e-63;
 Matches 343; Conservative 0; Mismatches 206; Indels 0; Gaps 0;
 QY 118 GAGCCCTCCATCTCCAAGGAGATCATGACCTTCAACACACCAAGCACCACCTACGACTTAT 177
 Db 1 GAACCTGCTTCTGGGGGAGATAATGGAGACGACTACGAGAAGCACCAACCCACCTAC 60
 QY 178 GTTAACGGCTCAACGCTGCGAGGAGGAGTATCTGGCGCGCTGTGGCAAGGAGGATGTG 237
 Db 61 GTCAACAACCTGAACGCGCGGAGGACAAGCTGATCGACGCTCCCGCAGCAGAGCCG 120
 QY 238 CTTACCCAGGTTAAGCTTCACTCTGCTTCAAGTTCAACGAGGAGGAGCAGACATCAATCAC 297
 Db 121 CTCGGGAGATTCGCGAGCTGAACGCGGATCAANTTCAATTCGCGCGGTGGCCACATCAACAC 180
 QY 298 TCTCTGTTCTGGAAGAACTTGGCTCCCTATGATCCGAGGAGGCTACCTCTCTGAAGGA 357
 Db 181 TCGCTCTTCTGGAAGAACTTGGCTCCGCGCGACAAACAGGGCGCGGAGCTCGACTCGGC 240
 QY 358 CCTCTCAAGAGGCTATCGAGGAATCTTTTGGTTCTTTTCGAGGCTTTCAGAGAGAGTTTC 417
 Db 241 GAGCTGCGCTCCGCGATCGACCGCGACTTTTGGCTCGCTCGACGCAATGAAGGAGAGTTTC 300
 QY 418 AAGCTGACACCGCTGCTGTCAGAGATCCGATCGGGCTGGCTTGGCTTGAACCCGCTT 477
 Db 301 AACGCGCGCTCGCGGATCCAGGGTATCGGCTGGGGCTGGCTCGGCTGGAACCCGACG 360
 QY 478 ACTAAGAGCTGGAAGTCAACACGAGCGGCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 537

Db 361 ACGGAGAGTCGACATCATCAGCACCAGCGAACACAGGACCCGCTCCTGTCGCAAGCG 420
 QY 538 ATATCGAGATGACATCTGGGAGACCGTTCTTACCTTTCAGTCAAGAGCTCAAGCT 597
 Db 421 CTGATTCGATCGATCGCTGGGAGACCGTACTACCTGCACTAAGAGAGCTCAAGGCC 480
 QY 598 GACTATCTCGCTGCTGTTTGGTTCGCTTATCAACTACAAGGAGGAGAGGCCGCGATTGCG 657
 Db 481 GACTACTTCAAGCGCATCTGACCGCTGATCACTTTGAGGAGCGCGAGAGGCTCTCANG 540
 QY 658 GCTGCTCTC 666
 Db 541 GAGGCGCTC 549

RESULT 6

US-09-917-800A-1627
 ; Sequence 1627, Application US/09917800A
 ; Patent No. US20020119462A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mendrick, Donna
 ; APPLICANT: Porter, Mark
 ; APPLICANT: Johnson, Kory
 ; APPLICANT: Castle, Arthur
 ; APPLICANT: Elashoff, Michael
 ; APPLICANT: Gene Logic, Inc.
 ; TITLE OF INVENTION: Molecular Toxicology Modeling
 ; FILE REFERENCE: 44321-5038-US
 ; CURRENT APPLICATION NUMBER: US/09/917,800A
 ; CURRENT FILING DATE: 2001-07-31
 ; PRIOR APPLICATION NUMBER: US 60/222,040
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: US 60/222,880
 ; PRIOR FILING DATE: 2000-11-02
 ; PRIOR APPLICATION NUMBER: US 60/290,029
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: US 60/290,645
 ; PRIOR FILING DATE: 2001-05-15
 ; PRIOR APPLICATION NUMBER: US 60/292,336
 ; PRIOR FILING DATE: 2001-05-22
 ; PRIOR APPLICATION NUMBER: US 60/295,798
 ; PRIOR FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: US 60/297,457
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/298,884
 ; PRIOR FILING DATE: 2001-06-19
 ; PRIOR APPLICATION NUMBER: US 60/303,459
 ; PRIOR FILING DATE: 2001-07-09
 ; NUMBER OF SEQ ID NOS: 1740
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1627
 ; LENGTH: 1492
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_017051
 US-09-917-800A-1627

Query Match 30.6%; Score 205; DB 9; Length 1492;
 Best Local Similarity 62.5%; Pred. No. 8.6e-58;
 Matches 363; Conservative 0; Mismatches 200; Indels 18; Gaps 2;
 QY 69 CAGGCAAGCATACCTGCTGAGCTTCTTACGCTTACGATGCGCTGGAGCCCTCCAT 128
 Db 134 CCGGCACAGACAGCTCTCTGACCTTACGACTATGCGCTGGAGCCGACAT 193
 QY 129 CTCGAAGAGATCATGACCCCTTACACACCAAGACCATCATGATTTATGTTAAGGCT 188
 Db 194 TAAACGCGAGATCATGACCTGACCAACAGCAAGACCAACGCGACCTACGTGAACAATCT 253
 QY 189 CAACTGCGGAGGAGTACTCGCCGCTGCGAGGAGGATGCTTACCCAGT 248

Db 254 GAACGTCACCGAGGAGAGTATCACAGAGCGCTGCGCAAGGAGATGTTACAACTCAGT 313
 QY 249 TAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGACACATCAATCACTCTCTGTTCTG 308
 Db 314 TGCTCTTCAGCTGACCTGAAGTTCAATGGCGGGGCCATATCAATCACAGATTTCTG 373
 QY 309 GAAGAACTTGGTCCCTATGGATCCGAGAGGCTACCCCTCTCTGAAGGACCTCTCAAGAA 368
 Db 374 GACAACTGAGCCCTAAGGGTGGTGGAGAACCCCA-----AAGGAGAGTTGCTGA 424
 QY 369 GCTATCAGAGATCTTTTGGTCTTTTCGAGGCTTCAAGAGAGAGTTCAAGCTGACAC 428
 Db 425 GCTATCAAGCGTGAATTTGGTCTTTTGAAGTTTAAAGGAGAACTGACAGCTGTGTC 484
 QY 429 CGCTGCTGTCCAAGGATCGGATGGGCTTGGCTTGAACCCGCTTACTAAGAAGCT 488
 Db 485 TGTGGAGTCCAAGTTTCAAGCTGGGCTGGCTTGGCTTCAATAGGAGCAAGTTCGTT 544
 QY 489 GGAAGTCAACGACCGCCCAACAGGACCCCTTGTG-----TTACTCACATTCCTAT 539
 Db 545 ACAGATTGCGGCTGCTCTAATCAGGACCCACTGCAAGGAACACACAGGCTTATTCCT 604
 QY 540 CATCGAGTTGACATCTGGGAGCAGCTTTCTACCTTCAGTACAGAGAGCTCAAGCTCA 599
 Db 605 GCTGGGATGATGTGTGGGAGCAGCTTACTTCTCAGTATATAAAACGTCAGACCTGA 664
 QY 600 CTATCTGCTGCTGTTTGGTCCGTTTATCAACTACAAGGAGG 640
 Db 665 CTATCTGAAGCCATTTGGAATGATCAACTGGGAGATG 705

RESULT 7

US-10-424-599-90405/c
 ; Sequence 90405, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 90405
 ; LENGTH: 987
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MBT3847_52648C.1
 US-10-424-599-90405

Query Match 30.3%; Score 202.8; DB 12; Length 987;
 Best Local Similarity 61.1%; Pred. No. 4e-57;
 Matches 352; Conservative 0; Mismatches 212; Indels 12; Gaps 1;
 QY 78 GCATACCTGCTGAGCTTCTTACGCTTACGATGCGCTGGAGCCCTCCATCTCCAAGGA 137
 Db 806 GTACACGTTACCCGATCTGGATTACGACTATGCGGACCTGGAGCAGCATCAGCGGCA 747
 QY 138 GATCATGACCTTCCACCACCAAGCAGCATCAGACTTATGTATACGGGCTCAAGCGTGC 197
 Db 746 CATCATGAGCTGACCCACCAAGCAGCAGCAGCTTACATCACCACACTACAAGGC 687
 QY 198 CAGAGAGAGTACTCGGCGCTGTGGGCAAGAGAGATGCTTACCAGGTTAAGCTTCA 257
 Db 686 CTTGAGCAGCTCCAAAGACGCCATCGCCAAAGAAAGATTCTCCCGCGTGTAAAGTCCA 627
 QY 258 GTCTGCTCTCAAGTTCAAGGAGGAGGACACATCAATCACTCTCTGTTCTGGAAGACTT 317
 Db 626 GGGCGCCATCAAGTTCAACGGGAGGATCATGTCAACCATCTATTTCTGAAAAATCT 567


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489 GGAAGTCAACGACCGCAACCAAGGACCCCTCTGCTTACT-----CACATTCTCTAT 539
      |||      |||      |||      |||      |||      |||      |||      |||
570 ACAAAATGCTGTTGTCACAAATCAGGATCCACTGCAAGGAACAACAGGCGCTTATTCCACT 629
      |||      |||      |||      |||      |||      |||      |||      |||
540 CATCGGAGTTACATCTCGGGACGACGCTTTCTACCTTCAGTACAAGACGTCAAGCCTCA 599
      |||      |||      |||      |||      |||      |||      |||      |||
630 GCTGGGGATTGATGTGGGAGCAGCTTACTACCTTCAGTTAAAAATGTGAGGCGCTGA 689
      |||      |||      |||      |||      |||      |||      |||      |||
600 CTATCTCGCTGCTGTTTGGTTCGGTTATCAACTACAAGGAGGAGGCGGCCGATTGCAGCG 659
      |||      |||      |||      |||      |||      |||      |||      |||
690 TTATCTAAAAGCTATTGGAATGTAATCAACTGGGAGAATGTAACCTGAAAGATACATGCG 749
      |||      |||      |||      |||      |||      |||      |||      |||
QY      660 T 660
Db      750 T 750

RESULT 10
US-10-198-846-13503
; Sequence 13503, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13503
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13503

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RESULT 11

US-09-954-456-1822

; Sequence 1822, Application US/09954456

; Patent No. US20020115057A1

; GENERAL INFORMATION:

; APPLICANT: Young, Paul

; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents

; TITLE OF INVENTION: Sets

; FILE REFERENCE: 689290-76

; CURRENT APPLICATION NUMBER: US/09/954,456

; CURRENT FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: US/60/233,617

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US/60/234,052

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: US/60/234,923

; PRIOR FILING DATE: 2000-09-25

; PRIOR APPLICATION NUMBER: US/60/235,134

; PRIOR FILING DATE: 2000-09-25

; PRIOR APPLICATION NUMBER: US/60/235,637

; PRIOR FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US/60/235,638

; PRIOR FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US/60/235,711

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: US/60/235,720

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: US/60/235,840

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: US/60/235,863

; PRIOR FILING DATE: 2000-09-27

; NUMBER OF SEQ ID NOS: 2276

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1822

; LENGTH: 1026

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-954-456-1822

Query Match	29.6%;	Score 197.8;	DB 14;	Length 996;
Best Local Similarity	60.9%;	Pred. No. 1.9e-55;		
Matches 366;	Conservative 0;	Mismatches 217;	Indels 18;	Gaps 2
Qy	69	CAGGCGAAGCATACCTGCCTGAGCTTCCTTACGCTTACGATGCCCTGGAGCCCTCCAT	128	
Db	156	CAGGCGAAGCACACGCTCCCGACCTCCCTTACGACTACGCGCGCCCTGGAACTTCACAT	215	
Qy	129	CTCCAAGGAGATCATGACCCCTTACCACCAAGCACCATCAGACTTATGTATTAAAGGCT	188	
Db	216	CAACGCGGAGATCATGCGCTGCACCAAGACACCAACGCGGCTACGTGAACAACCT	275	
Qy	189	CAACGCTCCGAGGAGAGCTACTCGCGCCCTGTGGCGAAGGAGTAGTGCTTACCCAGGT	248	
Db	276	GAACGTCAACGAGGAGAAGTACCAGGAGCGGTGSCCAAGGGAGATGTTTACAGCCAGAT	335	
Qy	249	TAAGCTTCAGTCTGCTCTCAAGTTCAACGAGGAGGACACATCAATCACTCTCTGTTCTG	308	
Db	336	AGCTCTTCAGCCTCGCATGAACTTCAATGGTGGTGCATATCAATCAATPAGCAITTTCTG	395	
Qy	309	GAAGAACCTTGGCTCCCTATGGATCGAGAGGCTACCCCTCTCTGAAGAGACCTCTCAAGAA	368	
Db	396	GACAAACCTTCAGCCCTAACCGTGGTGGAGAACCCA-----AAGGGAGTTGCTGGA	446	
Qy	369	GGCTATCGAGGAATCTTTTGGTTCTTTTCAGAGCCCTTCAAGAGAAGTGTCAACGCTGCAC	428	
Db	447	AGCCATCAACGCTGACTTTGGTTCTTTGACAAGTTTAAAGAGAAGCTCACGCTGCATC	506	
Qy	429	CGTCTGCTGTCCAAGGATCCGGATGGGGCTTGGCTTGGTTGAACCCCGTTACTTAAGAAGCT	488	


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QY 69 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 129 CTCGAGAGATCATGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 188
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 189 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 248
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 249 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 308
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 309 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 368
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 369
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 369 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 428
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 429
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 429 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 488
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 489
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 489 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 539
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 540 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 599
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 600
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 600 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 659
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 660
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 660 T 660
   |||
Db 661 T 661

```

RESULT 14

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US-10-198-846-13787
; Sequence 13787, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13787
; .LENGTH: 2825
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13787

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Query Match 29.6%; Score 197.8; DB 14; Length 2825;
Best Local Similarity 60.9%; Pred. No. 2.9e-55;

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Matches 366; Conservative 0; Mismatches 217; Indels 18; Gaps 2;
QY 69 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 215 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 274
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 129 CTCGAGAGATCATGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 188
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 334
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 189 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 248
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 394
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 249 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 308
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 395 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 454
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 309 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 368
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 505
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 369 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 428
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 506 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 565
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 429 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 488
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 566 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 625
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 489 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 539
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 626 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 685
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 540 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 599
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 686 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 745
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 600 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 659
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 746 CAGGCAAGCATACCCCTGCTGAGCTTCCCTTACGATGCGCTGGAGCCCTCCAT 805
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 660 T 660
   |||
Db 806 T 806

```

RESULT 15

```

US-09-770-445-745
; Sequence 745, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana

```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2004, 17:09:18 ; Search time 60 Seconds
(without alignments)
1045.426 Million cell updates/sec

Title: US-09-727-855B-5
Perfect score: 1153
Sequence: 1 MSVRSLSSVSRQTFVAPAA.....AAWSVINYKEARLQAAL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	692	60.0	224	2 AAW29771	Aaw29771 Malassezia
2	668.5	58.0	206	2 AAW29770	Aaw29770 Malassezia
3	634.5	55.0	222	7 ADD45869	Add45869 Rat Prote
4	623	54.0	222	2 AAW98170	Aaw98170 Human nat
5	623	54.0	222	3 AAB08204	Aab08204 Amino aci
6	621	53.9	222	2 AAR44801	Aar44801 MnSOD cdn
7	621	53.9	222	2 AAR30713	Aar30713 Human man
8	621	53.9	222	2 AAW00018	Aaw00018 Human man
9	621	53.9	222	2 AAW98169	Aaw98169 Human nat
10	620	53.8	222	2 AAW98175	Aaw98175 Human man
11	619	53.7	222	1 AAP17101	Aap17101 Recombina
12	619	53.7	223	1 AAP80551	Aap80551 Human man
13	618	53.6	222	2 AAW00453	Aaw00453 Human man
14	618	53.6	222	2 AAW98171	Aaw98171 Human man
15	618	53.6	222	2 AAW98174	Aaw98174 Human man
16	618	53.6	222	2 AAW98173	Aaw98173 Human man
17	618	53.6	222	3 AAB08205	Aab08205 Q143N mod
18	617	53.5	222	2 AAR61337	Aar61337 Human man
19	617	53.5	222	2 AAW96317	Aaw96317 Human man
20	617	53.5	222	2 AAW82446	Aaw82446 Human mSO
21	617	53.5	222	2 AAW98172	Aaw98172 Human man
22	617	53.5	222	3 AAW98206	Aaw98206 A modifie
23	616	53.4	222	2 AAW98176	Aaw98176 Human man
24	616	53.4	222	5 ABB79798	Abb79798 Human man
25	616	53.4	222	5 ABB07330	Abb07330 Human man

ALIGNMENTS

RESULT 1

AAW29771	AAW29771 standard; protein; 224 AA.
XX	AAW29771;
XX	AC
XX	27-AUG-2003 (revised)
DT	23-FEB-1998 (first entry)
XX	XX
DE	Malassezia fungus MF-4 antigenic protein.
XX	XX
KW	Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;
KW	allergy; antigen.
XX	Malassezia.
OS	Malassezia.
XX	XX
PN	WO9721817-A1.
XX	XX
PD	19-JUN-1997.
XX	XX
PF	10-DEC-1996; 96WO-JP003602.
XX	XX
PR	12-DEC-1995; 95JP-00346627.
PR	05-SEP-1996; 96JP-00257612.
XX	05-SEP-1996; 96JP-00257613.
PA	(TAKI) TAKARA SHUZO CO LTD.
XX	XX
PI	Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
PI	Akiyama K, Yasueda H, Yamaguchi H;
XX	XX
DR	WPI; 1997-332788/30.
DR	N-PSDB; AAT85877.
XX	XX
PT	Antigenic proteins from the fungus Malassezia - bind to IgE antibodies
PT	present in patients with Malassezia allergies, useful for diagnosis,
PT	treatment and prevention of such conditions.
XX	XX
PS	Claim 38; Page 85-86; 162pp; Japanese.
XX	XX
CC	The present sequence represents a specifically claimed antigenic protein
CC	isolated from the fungus Malassezia. The antigenic protein can bind to
CC	IgE antibodies present in patients with allergic conditions. Antigenic
CC	proteins, peptides and nucleic acids from the fungus Malassezia can be
CC	used in the diagnosis, treatment and prevention of allergic conditions
CC	due to Malassezia organisms (such as M.furfur, M. sympodialis and
CC	M.pachydermatitis). (Updated on 27-AUG-2003 to correct OS field.)
XX	XX

```
SQ Sequence 224 AA;
Query Match 60.0%; Score 692; DB 2; Length 224;
Best Local Similarity 59.3%; Pred. No. 5.4e-66;
Matches 128; Conservative 31; Mismatches 53; Indels 4; Gaps 1;
QY 11 SROTFFVAP---AAFOIRAKHTLPPLPYADALEPSISKEIMTLHHTKHQTYVNGLNAA 66
DQ 6 TRRAAAPLANAAQMGVETKTLPLPYDYGALPEAISGEIMETHYKHKHTYVNNLNA 65
QY 67 EESYSAAGKEDVLTQVKLSALKFNGGGHINHSFWKNLAPYSGSEATLSEGPLKKAIE 126
DQ 66 EDKLIDALPOQSLGEIAQLNAIKFNGGGHINHSFWKNLAPYSGSEATLSEGPLKKAIE 125
QY 127 ESFGSFEAFKKENADTAAGVSGWGLGNPLTKLEVTITANQDPLLTTHPIIGVDIW 186
DQ 126 RDFSVDAMKEFNAALAGIQSGWGLGNPLTKLEVTITANQDPLLTTHPIIGVDIW 185
QY 187 EHAFYLOYNKVPDYLAAVWSVINYKEAEARLQAL 222
DQ 186 EHAFYLOYNKVPDYLAAVWSVINYKEAEARLQAL 221
RESULT 2
ID AAW29770 standard; protein; 206 AA.
XX AC AAW29770;
XX DT 27-AUG-2003 (revised)
XX DT 23-FEB-1998 (first entry)
XX DE Malassezia fungus MF-3 antigenic protein.
XX KW Malassezia; fungus; antigenic; human; IgE; immunoglobulin E; antibody;
XX KW allergy; antigen.
XX OS Malassezia.
XX PN WO9721817-A1.
XX PD 19-JUN-1997.
XX PF 10-DEC-1996; 96WO-0003602.
XX PR 12-DEC-1995; 95JP-00346627.
XX PR 05-SEP-1996; 96JP-00257612.
XX PR 05-SEP-1996; 96JP-00257613.
XX PA (TAKI ) TAKARA SHUZO CO LTD.
XX PI Takesako K, Okado T, Yagihara T, Kuroda M, Onishi Y, Kato I;
XX PI Akiyama K, Yasueda H, Yamaguchi H;
XX WPI; 1997-332788/30.
XX N-PSDB; AAT85876.
XX PT Antigenic proteins from the fungus Malassezia - bind to IgE antibodies
XX PT present in patients with Malassezia allergies, useful for diagnosis,
XX PT treatment and prevention of such conditions.
XX PS Claim 36; Page 83-84; 162pp; Japanese.
XX CC The present sequence represents a specifically claimed antigenic protein
XX CC isolated from the fungus Malassezia. The antigenic protein can bind to
XX CC IgE antibodies present in patients with allergic conditions. Antigenic
XX CC proteins, peptides and nucleic acids from the fungus Malassezia can be
XX CC used in the diagnosis, treatment and prevention of allergic conditions
XX CC due to Malassezia organisms (such as M.furfur, M. sympodialis and
XX CC M.pachydermatidis). (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 206 AA;
Query Match 58.0%; Score 668.5; DB 2; Length 206;
Best Local Similarity 63.1%; Pred. No. 1.7e-63;
Matches 123; Conservative 24; Mismatches 47; Indels 1; Gaps 1;
QY 23 IRAKHTLPPLPYADALEPSISKEIMTLHHTKHQTYVNGLNAAEESYSAAGKEDVLTQ 82
DQ 3 VMTYTLPLPLPYADALEPFSKIMTVHDDKHQTYVNNLNAAKAYAEATAANDVLKQ 62
QY 83 VKLSALKFNGGGHINHSFWKNLAPYSGSEATLSEGPLKKAIEBSFGSFEAFKKFNAD 142
DQ 63 IQLSALKFNGGGHINHSFWKNLAPYSGGGQLNDGPLKQALIEGFDFEKFKTFTNTK 122
QY 143 TAAVQSGWGLGNPLTKLEVTITANQDPLLTTHPIIGVDIWEHAPYLOYNKVPDY 202
DQ 123 AAGIQSGWGLGVAP-TGNLDLVVAKDQDPLTTHHPVIGWDGWEHAWYLOYNKASYL 181
QY 203 AAVWSVINYKEAEAR 217
DQ 182 KAWNVVNVNAEAEKR 196
RESULT 3
ADD45869
ID ADD45869 standard; protein; 222 AA.
XX AC ADD45869;
XX DT 29-JAN-2004 (first entry)
XX DE Rat Protein CAA39937, SEQ ID NO 11539.
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO ) GEN HOSPITAL CORP.
XX PA (FARB ) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENEANK; CAA39937.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
```

method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 222 AA;

Query Match 55.0%; Score 634.5; DB 7; Length 222;
 Best Local Similarity 55.4%; Pred. No. 8.7e-60;
 Matches 123; Conservative 30; Mismatches 58; Indels 11; Gaps 4;
 QY 1 MSVRASLSVSRQTFVAPAAAFQI--RAKHTLPYAYDALEPSISKEIMTLHHTKHOT 58
 Db 1 MLCRAACSGRR---LGPRASTAGSRKHSPLDLYDGALEPHINAQIMQLHRSKHAT 57
 QY 59 YVNGLNAAEESYSAAYGKEDVLTQVKLSALKFNGGGHINHSFWKNLAPYGSSEATLSE 118
 Db 58 YVNNLVNTEKYHEALAKGDVTTQVALQPALEKFGGGHINHSIFWNLSPKGGGE---PK 114
 QY 119 GPLKKAIESFGSFAPKFKFNADTAAGVSGGHWGLNPLTKKLEVTNTANQDPL---L 175
 Db 115 GELLEAKRDFSGFEKFKELTAVSVGVQSGGHWGLFNKEQGRLOIAACSNQDPLQGT 174
 QY 176 THPIIGVDIWEHAFYLYQKNVKPDYLAAVWSVINYKEAEAR 217
 Db 175 GLIPLGIDWEHAFYLYQKNVRPDYLAALWNVINWENVSQR 216

RESULT 4

AAW98170
 ID AAW98170 standard; protein; 222 AA.

XX AAW98170;

XX 05-JUL-1999 (first entry)

XX Human native manganese superoxide dismutase.

XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
 KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
 KW inflammation; reperfusion injury; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /note= "signal peptide"
 FT Protein 25..222
 FT /note= "mature protein"
 FT Active-site 50
 FT /note= "His-26"
 FT Active-site 54
 FT /note= "His-30"
 FT Active-site 58
 FT /note= "Tyr-58"
 FT Active-site 98
 FT /note= "Tyr-74"
 FT Misc-difference 155
 FT /label= Gln, Glu
 FT Active-site 167
 FT /note= "Gln-143"
 FT Active-site 183
 FT /note= "Asp-159"
 FT Active-site 185

FT Active-site /note= "Trp-161"
 FT 187
 FT /note= "His-163"
 XX
 XX WO9913088-AL.
 XX 18-MAR-1999.
 XX
 XX 10-SEP-1998; 98WO-US018842.
 XX
 XX 10-SEP-1997; 97US-00927230.
 XX
 XX (UYFL) UNIV FLORIDA.
 XX
 XX Nick HS, Silverman DN;
 XX
 XX WPI; 1999-229242/19.
 XX
 XX New recombinant human manganese superoxide dismutase proteins.
 XX
 XX Claim 2; Page 53-54; 61pp; English.

PS This protein is human manganese superoxide dismutase (hMnSOD). Novel
 CC hMnSOD proteins having catalytic activity which differs from this natural
 CC hMnSOD are claimed (see AAW98171-77). The modified proteins exhibit
 CC reduced or no product inhibition, or have greater activity, or both,
 CC compared to natural hMnSOD. The modifications involve one or amino acid
 CC substitutions within the active site of the enzyme, especially at
 CC residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and
 CC His-163. The modified hMnSOD, or expression vectors in which modified
 CC hMnSOD nucleic acid is linked to a promoter (preferably mammalian), can
 CC be used to protect a cell line from damage caused by superoxide radicals
 CC (claimed). They can also be used to treat subjects suffering from, or at
 CC risk of, cytotoxicity caused by superoxide radicals (claimed). As such,
 CC they can be used as antioxidants in the treatment of a variety of
 CC disorders, including inflammation (claimed), reperfusion injury following
 CC ischemia (claimed), and cellular damage caused by chemotherapeutic agents
 XX
 XX Sequence 222 AA;

Query Match 54.0%; Score 623; DB 2; Length 222;

Best Local Similarity 53.6%; Pred. No. 1.5e-58;

Matches 118; Conservative 31; Mismatches 61; Indels 10; Gaps 4;

QY 6 SLSSVSRTFVAPAAAFQI--RAKHTLPYAYDALEPSISKEIMTLHHTKHOTYVNG 63
 Db 5 AVCGTSRQ--LAPALYGLSGRQKHSPLDLYDGALEPHINAQIMQLHSHKHAAYVNN 62
 QY 64 NAAEESYSAAYGKEDVLTQVKLSALKFNGGGHINHSFWKNLAPYGSSEATLSEGLKK 123
 Db 63 NVTEEKYQELAKGDVTAQIALQPALEKFGGGHINHSIFWNLSPNGGGE---PKGELLE 119
 QY 124 ATEESFGSFEAFKFKFNADTAAGVSGGHWGLNPLTKKLEVTNTANQDPL---LTHIPT 180
 Db 120 AIKRDGSGDFKFKELTAAASVGVQSGGHWGLFNKXRAHLQIAACPNQDPLQGTGLIPL 179
 QY 181 IGVDIWEHAFYLYQKNVKPDYLAAVWSVINYKEAEARLOA 220
 Db 180 LGIDVWEHAFYLYQKNVRPDYLAALWNVINWENVTERYMA 219

RESULT 5

AAB08204
 ID AAB08204 standard; protein; 222 AA.

XX AAB08204;

XX 04-DEC-2000 (first entry)

XX Amino acid sequence of a human manganese superoxide dismutase.

DE Human; manganese superoxide dismutase; hMn SOD; superoxide radical;
 KW superoxide radical damage; cytotoxicity; inflammation; ischemia;

AC AAR90713;
 XX 25-MAR-2003 (revised)
 DT 06-APR-1996 (first entry)
 DT
 XX Human manganese superoxide-dismutase.
 DE
 XX Human; manganese superoxide-dismutase; T-lymphocyte; probe; cDNA;
 KW Escherichia coli; plasmid pMS8-4; N-terminal truncation; cloning;
 KW aminopeptidase; antiinflammatory; oxygen free radical scavenger;
 KW synovial inflammation; arthritis; lung fibrosis.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..24 "Pre-peptide"
 FT /note= "39..48"
 FT Region /note= "Region used to construct probe AAT15591"
 FT Misc-difference 66
 FT /note= "Gln in previously published sequence"
 FT Misc-difference 112
 FT /note= "Gln in previously published sequence"
 FT Misc-difference 132
 FT /note= "Gln in previously published sequence"
 FT Misc-difference 147..148
 FT /note= "Residues not present in previously published sequence"
 FT Region 203..213
 FT /note= "Region used to construct probe AAT15592"
 FT
 XX EP691401-A1.
 XX
 XX 10-JAN-1996.
 XX
 XX 25-MAR-1988; 95EP-00106995.
 XX
 XX 27-MAR-1987; 87US-00032734.
 PR
 PR 26-FEB-1988; 88US-00161117.
 XX
 XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
 PA
 XX Hartman JR, Beck Y, Nimrod A;
 XX WPI: 1996-059735/07.
 DR N-PSDB; AAT15589.
 XX
 XX New human manganese superoxide dismutase analogues - having a Lys and
 PT opt. His residue absent from the N-terminus, useful for treating e.g.
 PT synovial inflammation, arthritis or lung fibrosis.
 XX
 XX Example 1; Fig 1; 45pp; English.
 PS
 XX The sequence represents a human manganese superoxide-dismutase (MnSOD),
 CC and is encoded by a human T-lymphocyte cDNA isolated from a library in
 CC phage lambda-gt10 in Escherichia coli, by screening with a 5'-probe
 CC (AAT15591) and a 3'-probe (AAT15592), followed by subcloning in plasmid
 CC pBR322 to give plasmid pMS8-4. The cDNA may be expressed in e.g. E. coli
 CC for production of recombinant MnSOD. The MnSOD product may be cleaved
 CC with Aeromonas proteolytica aminopeptidase to produce an N-terminally
 CC truncated analogue with lysine and optionally histidine residues removed.
 CC The MnSOD analogue may be used in therapy of conditions associated with
 CC generation of oxygen free radicals, particularly synovial inflammation,
 CC arthritis and lung fibrosis (claimed). (Updated on 25-MAR-2003 to correct
 CC PF field.)
 XX
 SQ Sequence 222 AA;
 Query Match 53.9%; Score 621; DB 2; Length 222;
 Best Local Similarity 53.8%; Pred. No. 2.5e-38;
 Matches 118; Conservative 31; Mismatches 61; Indels 10; Gaps 4;
 QY 6 SLSSVSRSQTFVAPAAFG1--RAKHHTLPYDALEPSISKIMTLHHTKHQTYVNGL 63

Db 5 AVCGTSRQ--LAPALGVLSRQKHSPLDLPYDYGALPHINAQIMQLHSHKHAAYNNL 62
 QY 64 NAAEESYSAAGKEDVLTVQVLOSALKFNGGGHINSHLFWKNLAPYGSEATISEGLPKK 123
 Db 63 NVTEERYQAEALAKGDVTAQIALQPALKFNGGGHINSHLFWKNLSPNGGGE---PKGELLE 119
 QY 124 AIEESFGSFEAFKFKFNADTAAGVSGSGWGLGNPLTKKLEVTITANODPL---LTHIPI 180
 Db 120 AIKRDGSEDFKREKUTAAASVGVSGSGWGLGNKORHGLQIAACPNQDPLQGTGLIPL 179
 QY 181 IGVDIWEHAFYLOYNKVPDYLAAMVMSVINYKEAEARLQA 220
 Db 180 LGIDVWEHAYLYQKNVRPDYLAAMVMSVINYKEAEARLQA 219
 RESULT 8
 AAW00018
 ID AAW00018 standard; protein; 222 AA.
 XX
 AC AAW00018;
 XX
 DT 25-MAR-2003 (revised)
 DT 24-OCT-1996 (first entry)
 XX
 DE Human manganese superoxide dismutase.
 XX
 KW Manganese superoxide dismutase; MnSOD; reperfusion injury; ischaemia;
 KW bronchial pulmonary dysplasia; inflammation; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= Sig_peptide
 FT Protein 25..222
 FT /label= Mat_protein
 XX
 PN US5540911-A.
 XX
 XX 30-JUL-1996.
 XX
 XX 09-JAN-1995; 95US-00370461.
 XX
 XX 22-NOV-1985; 85US-00801090.
 PR 12-SEP-1986; 86US-00907051.
 PR 29-OCT-1986; 86IE-00002851.
 PR 27-MAR-1987; 87US-00032734.
 PR 13-DEC-1989; 89US-00453057.
 PR 10-JUL-1992; 92US-00912213.
 PR 14-SEP-1993; 93US-00120951.
 XX
 XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
 PA
 XX Hartman JR, Beck Y;
 PI WPI: 1996-361912/36.
 DR N-PSDB; AAT34277.
 XX
 XX Use of recombinant human manganese superoxide dismutase - for treating
 PT inflammation or bronchial pulmonary dysplasia, reducing reperfusion
 PT injury or prolonging organ survival.
 XX
 PS Claim 1; Fig 1A-1C; 27pp; English.
 XX
 XX Human manganese superoxide dismutase (MnSOD) (AAW00018) catalyses the
 CC reduction of superoxide radicals to H2O2 and O2. Recombinant MnSOD can be
 CC obtd. using transformed host cells, esp. Escherichia coli cells contg. a
 CC plasmid carrying e.g. a cDNA clone (AAT34277) obtd. from a human T-cell
 CC library. The MnSOD is useful for reducing reperfusion injury, treating
 CC inflammation or bronchial pulmonary dysplasia and for prolonging survival
 CC of excised organs. (Updated on 25-MAR-2003 to correct PF field.) (Updated
 CC on 25-MAR-2003 to correct PR field.)

Db 180 LGIDVWEHAYLYQKNVRPDLKAIWNVINWENVTERYMA 219

RESULT 14

AAW98171
ID AAW98171 standard; protein; 222 AA.

XX AAW98171;
AC
XX 05-JUL-1999 (first entry)
XX Human manganese superoxide dismutase Q143N mutant.
XX
XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
KW inflammation; reperfusion injury; therapy; mutant.
XX

OS Homo sapiens.
XX Synthetic.

Key	Location/Qualifiers
Peptide	1..24 "signal peptide"
Protein	25..222
Active-site	/note= "mature protein"
Active-site	50
Active-site	/note= "His-26"
Active-site	54
Active-site	/note= "His-30"
Active-site	58
Active-site	/note= "Tyr-58"
Active-site	98
Active-site	/note= "Tyr-74"
Misc-difference	155
Misc-difference	/label= Gln, Glu
Active-site	/note= "Gln replaces Asn in wild-type hMnSOD"
Active-site	167
Active-site	/note= "Gln-143"
Active-site	183
Active-site	/note= "Asp-159"
Active-site	185
Active-site	/note= "Trp-161"
Active-site	187
Active-site	/note= "His-163"

WO9913088-A1.

18-MAR-1999.

10-SEP-1998; 98WO-US018842.

10-SEP-1997; 97US-00927230.

(UYFL) UNIV FLORIDA.

Nick HS, Silverman DN;

WPI; 1999-229242/19.

New recombinant human manganese superoxide dismutase proteins.

Claim 15; Page 54-55; 61pp; English.

This protein is a Q143N mutant of human manganese superoxide dismutase (hMnSOD, see also AAW98170). Novel modified hMnSOD proteins having catalytic activity which differs from natural hMnSOD are claimed. The modified proteins (see also AAW98172-77) exhibit reduced or no product inhibition, or have greater activity, or both, compared to natural hMnSOD. The modifications involve one or amino acid substitutions within the active site of the enzyme, especially at residues His-26, His-30, Tyr-34, His-74, Gln-143, Asp-159, Trp-161 and His-163. Gln-143, Tyr-34 and His-30 are located near the active site metal, are highly conserved, and

are involved in a hydrogen bond relay which links the active site metal-bound hydroxyl group to ordered solvent, and are thus all potentially involved in catalytic activity, product inhibition and/or enzyme stability. The particularly preferred Q143N mutant has a k_{cat} of 0.3 m/sec and a k_{cat}/K_m of 0.82/ μ M/sec compared to respective values of 40 m/sec and 800/ μ M/sec for wild-type hMnSOD. It exhibits no product inhibition. Modified hMnSODs, or expression vectors in which a modified hMnSOD nucleic acid is linked to a promoter (preferably mammalian), are used to protect a cell line from damage caused by superoxide radicals (claimed). They can also be used to treat subjects suffering from, or at risk of, cytotoxicity caused by superoxide radicals (claimed). As such, they can be used as antioxidants in the treatment of a variety of disorders, including inflammation (claimed), reperfusion injury following ischemia (claimed), and cellular damage caused by chemotherapeutic agents (claimed).

XX Sequence 222 AA;

Query Match 53.6%; Score 618; DB 2; Length 222;

Best Local Similarity 53.2%; Pred. No. 5.3e-58;

Matches 117; Conservative 31; Mismatches 62; Indels 10; Gaps 4;

Qy 6 SLSSVSRQTEVAPAFQI--RAKHTELPYADALEPSISKEIMTLHHTKHQTYNGL 63

Db 5 AVCGTSRQ--LAPALGYLGRQKHSPLDLPDYGALEPHINAQIMQLHSHKHAAYVNNL 62

Qy 64 NAARESYRAAGKEDVLTQVKLQSKALFKGGGHHNSLFWKNLAPYGEATLSEGLPKX 123

Db 63 NVTREKYQEAALARGDVTAQIALQFALPKFGGGHHNSIFWTNLSPNGGGE---PKGELLE 119

Qy 124 AIBESFGSFEAFKKFNADTAAGVQSGGWGLNPLTKLEVTITANQDPL---LTHIPI 180

Db 120 AIKRDGSGFDKFKELTAASGVQSGGWGLNPKYKRAHLQIAACPNNDPLOGTTGLIPL 179

Qy 181 IGVDIWEHAFYLOYNKVPDYLAAVWSVINYKEAEAPLQA 220

Db 180 LGIDVWEHAYLYQKNVRPDLKAIWNVINWENVTERYMA 219

RESULT 15

AAW98174

ID AAW98174 standard; protein; 222 AA.

XX AAW98174;

XX 05-JUL-1999 (first entry)

XX Human manganese superoxide dismutase Q143D mutant.

XX Superoxide dismutase; MnSOD; SOD; human; protein engineering;
KW enzyme engineering; antioxidant; antiinflammatory; cytotoxicity;
KW inflammation; reperfusion injury; therapy; mutant.

XX Homo sapiens.

OS Synthetic.

Key	Location/Qualifiers
Peptide	1..24
Protein	/note= "signal peptide"
Active-site	25..222
Active-site	/note= "mature protein"
Active-site	50
Active-site	/note= "His-26"
Active-site	54
Active-site	/note= "His-30"
Active-site	58
Active-site	/note= "Tyr-58"
Active-site	98
Active-site	/note= "Tyr-74"
Misc-difference	155
Misc-difference	/label= Gln, Glu
Misc-difference	167
Active-site	/note= "Gln replaces Asp in wild-type hMnSOD"
Active-site	167

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2004, 17:09:18 ; Search time 22 Seconds
(without alignments)
520.953 Million cell updates/sec

Title: US-09-727-855B-5
Perfect score: 1153
Sequence: 1 MSVRASLSSVSRTQFVAPAA.....AAVWSVINYKEARLQAAL 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pdp.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pdp.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pdp.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pdp.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	692	60.0	224	4	US-09-091-097-8
2	668.5	58.0	226	4	Sequence 8, Appli
3	623	54.0	222	2	Sequence 6, Appli
4	623	54.0	222	3	Sequence 2, Appli
5	618	53.6	222	2	Sequence 2, Appli
6	618	53.6	222	2	Sequence 28, Appli
7	618	53.6	222	2	Sequence 3, Appli
8	618	53.6	222	3	Sequence 3, Appli
9	617	53.5	222	2	Sequence 28, Appli
10	617	53.5	222	2	Sequence 44, Appli
11	617	53.5	222	2	Sequence 52, Appli
12	610	52.9	198	6	Sequence 2, Appli
13	607	52.6	198	3	Patent No. 5240847
14	607	52.6	226	3	Sequence 2, Appli
15	606	52.6	198	6	Sequence 7, Appli
16	570	49.4	230	2	Patent No. 5240847
17	570	49.4	230	2	Sequence 30, Appli
18	536	46.5	177	6	Sequence 30, Appli
19	513.5	44.5	214	4	Patent No. 5240847
20	498.5	43.2	217	4	Sequence 75, Appli
21	496	43.0	204	1	Sequence 12227, A
22	495	42.9	204	1	Sequence 29, Appli
23	482.5	41.8	196	4	Sequence 17, Appli
24	479	41.5	200	4	Sequence 185, App
25	478.5	41.5	224	4	Sequence 2, Appli
26	465.5	40.4	201	4	Sequence 6654, Ap
27	462	40.1	233	2	Sequence 3584, Ap
					Sequence 31, Appli

Query Match 60.0%; Score 692; DB 4; Length 224;
Best Local Similarity 59.3%; Pred. No. 4.8e-73;

28 462 40.1 233 4 US-09-339-972-31
29 461 40.0 207 4 US-09-252-991A-24593
30 454.5 39.4 241 4 US-09-540-236-3442
31 444.5 38.6 207 4 US-09-214-909-24
32 430.5 37.3 188 4 US-09-262-856A-6
33 367 31.8 219 4 US-09-328-352-4346
34 358.5 31.1 205 4 US-09-543-681A-4456
35 349.5 30.3 227 4 US-09-489-039A-9633
36 337.5 29.3 245 4 US-09-252-991A-24333
37 326 28.3 214 3 US-09-411-578-1
38 326 28.3 214 4 US-09-749-233-1
39 312 27.1 190 4 US-08-679-493A-184
40 201.5 17.5 213 3 US-09-008-303-2
41 104 9.0 30 4 US-09-091-097-52
42 103.5 9.0 835 4 US-09-458-457-8
43 103.5 9.0 835 4 US-09-947-199A-8
44 93.5 8.1 2016 4 US-09-475-252-2
45 89.5 7.8 373 3 US-09-039-198A-14

ALIGNMENTS

RESULT 1
US-09-091-097-8
; Sequence 8, Application US/09091097
; Patent No. 6432407
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH
; APPLICANT: OKADO, TAKASHI
; APPLICANT: YAGIHARA, TOMOKO
; APPLICANT: KURODA, MASANOBU
; APPLICANT: ONISHI, YOSHIMI
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: AKIYAMA, KAZUO
; APPLICANT: YASUEDA, HIROSHI
; APPLICANT: YAMAGUCHI, HIDEYO
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
; TITLE OF INVENTION: MALASSEZIA
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,097
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0346P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-091-097-8

Sequence 31, Appli
Sequence 24593, A
Sequence 3442, Ap
Sequence 24, Appli
Sequence 6, Appli
Sequence 4346, Ap
Sequence 4456, Ap
Sequence 9633, Ap
Sequence 24333, A
Sequence 1, Appli
Sequence 184, App
Sequence 2, Appli
Sequence 52, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 14, Appli


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124 AIESFGSEAFKKFNADTAAVQSGSGWGLGNPLTKKLEVTTTANQDPL---LTHPI 180
Qy
120 AAKRDFSGDFKFKELTAASVQSGSGWGLGNPKKRAHLQAAACNQDPLQGTGLIPL 179
Db
181 IGVDIWEHAFYLYQKNVQKPDYLAAMVSVINYKEAEARLQA 220
Qy
180 LGIDVWEHAYLYQKNVQKPDYLAAMVSVINYKEAEARLQA 219
Db

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RESULT 4
US-09-151-052-2
; Sequence 2, Application US/09151052
; Patent No. 6107070
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 28 State Street, Floor 24
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/151,052
;

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PRIOR APPLICATION:
 PRIOR APPLICATION NUMBER: 08/927,230
 FILING DATE: September 10, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Remillard, Jane
 REGISTRATION NUMBER: 38, 872
 REFERENCE/DOCKET NUMBER: UPJ-001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 222 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: OTHER
 LOCATION: 131
 OTHER INFORMATION: Xaa can code for Gln or Glu

	Query Match	54.0%	Score 623;	DB 3;	Length 222;
	Best Local Similarity	53.6%;	Pred. No.	6.2e-65;	Matches 118; Conservative 31; Mismatches 61; Indels 10; Gaps 4;
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Dd	5 AVCGTSRQ-LAPALGYLSGRQRSHSLPDLPDYGALEPHINAQMQLHHSKHAHYVNVL	62	:	:	:
QY	64 NAAEESYSAAVGKDVLITOVKLQALKFNGGGCHINHSLFWNLAIPYGESEATLSGPGLKK	123	:	:	:
Dd	63 NVTEEKQEALAKGDVTQAIALQPALKFNFGGCHINHISFTWNLSPNGGGE---PKGELLE	119	:	:	:
QY	124 AIEESFCGSFAFKKFADNTAAGVSGSWGWLGLNPCLKLEVTTTANODPI-----LTTHPI	180	:	:	:
Dd	120 AIRDFCSGFDKFEKLTAASVGVGVSGSWGWLGNFRXKAHLQIAACPNQDPLQGTTGTLIPL	179	:	:	:
QY	181 IGVDIMEBHPYLQYNKYKPDIYAALVAWSVINNYKEAEARLQA	220	:	:	:

Db 180 LGIDVWEHAYLYQKNVRPDYLKAIWNVINWENVTERYMA 219

RESULT 5

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US-08-365-486A-28
; Sequence 28, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webeter, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-365-486A-28

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Query Match 53.6%; Score 618; DB 2; Length 222;
Best Local Similarity 53.6%; Pred. No. 2.4e-64;
Matches 118; Conservative 31; Mismatches 61; Indels

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QY	64	N	A	E	S	I	S	A	A	V	K	E	D	V	L	T	Q	V	L	Q	S	A	L	K	P	N	G	G	H	I	N	H	S	L	F	W	K	N	L	A	P	Y	O	S	E	A	T	I	S	E	G	P	L	K	123		
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QY	124	A	I	E	S	F	G	S	F	E	A	F	K	K	F	N	A	D	T	A	A	V	O	S	G	M	G	L	N	P	L	T	K	L	E	V	T	T	A	N	O	D	L	-	-	-	L	T	H	I	P	I	180				
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RESULT 6

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RESOLUTION 6
US-08-927-230A-3
; Sequence 3, Application US/08927230A
; Patent No. 5985633
; GENERAL INFORMATION:
; APPLICANT: Nick et al.
; TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
; NUMBER OF SEQUENCES: 11

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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, Floor 24
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,230A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: UFJ-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: OTHER
LOCATION: 131
OTHER INFORMATION: Xaa can code for Gln or Glu
US-08-927-230A-3

Query Match 53.6%; Score 618; DB 2; Length 222;
Best Local Similarity 53.2%; Pred. No. 2.4e-64;
Matches 117; Conservative 31; Mismatches 62; Indels 10; Gaps 4;

QY 6 SLSSVSRTFTVAPAAFI--RAKHTLPPLPAYDALEPSISKEIMTLHHTKHQTYVNGL 63
DB 5 AVCGTSRQ--LAPALGYLSRQKHSPLDIPYDGALEPHINAQIMQLHSHKHAAYVNNL 62
QY 64 NAAESYSAAVKGEDVLTQVKLSALKFNGGGHINHSIPWKNLAPYGSSEATLSGGLKK 123
DB 63 NVTEEKYQBALAKGDVTAQIALQPAKFKNGGGHINHSIPWNLSPNGGGE---PKGELLE 119
QY 124 AIEESFGSFEAPKKFNADTAAVQSGWGLGNPLTKKLEVTITANODPL---LTHIPI 180
DB 120 AIKRDGSGDFKFEKLTAAVQSGWGLGNPKKRAHLQIAACPNNDPLQGTGLIPL 179
QY 181 IGVDTWEHAFYLYQKNRPDYLAADVMSVINYKEAEARLQA 220
DB 180 LGIDVWEHAYLYQKNRPDYLAADVMSVINYKEAEARLQA 219

RESULT 7
US-09-151-052-3
Sequence 3, Application US/09151052
Patent No. 6107070
GENERAL INFORMATION:
APPLICANT: Nick et al.
TITLE OF INVENTION: Human Manganese Superoxide Dismutase Mutants
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Floor 24
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, Floor 24
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,230A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: UFJ-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: OTHER
LOCATION: 131
OTHER INFORMATION: Xaa can code for Gln or Glu
US-09-151-052-3

Query Match 53.6%; Score 618; DB 2; Length 222;
Best Local Similarity 53.2%; Pred. No. 2.4e-64;
Matches 117; Conservative 31; Mismatches 62; Indels 10; Gaps 4;

QY 6 SLSSVSRTFTVAPAAFI--RAKHTLPPLPAYDALEPSISKEIMTLHHTKHQTYVNGL 63
DB 5 AVCGTSRQ--LAPALGYLSRQKHSPLDIPYDGALEPHINAQIMQLHSHKHAAYVNNL 62
QY 64 NAAESYSAAVKGEDVLTQVKLSALKFNGGGHINHSIPWKNLAPYGSSEATLSGGLKK 123
DB 63 NVTEEKYQBALAKGDVTAQIALQPAKFKNGGGHINHSIPWNLSPNGGGE---PKGELLE 119
QY 124 AIEESFGSFEAPKKFNADTAAVQSGWGLGNPLTKKLEVTITANODPL---LTHIPI 180
DB 120 AIKRDGSGDFKFEKLTAAVQSGWGLGNPKKRAHLQIAACPNNDPLQGTGLIPL 179
QY 181 IGVDTWEHAFYLYQKNRPDYLAADVMSVINYKEAEARLQA 220
DB 180 LGIDVWEHAYLYQKNRPDYLAADVMSVINYKEAEARLQA 219

RESULT 8
US-08-880-342-28
Sequence 28, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

```

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ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,052
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/927,230
FILING DATE: September 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: UFJ-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: OTHER
LOCATION: 131
OTHER INFORMATION: Xaa can code for Gln or Glu
US-09-151-052-3

Query Match 53.6%; Score 618; DB 3; Length 222;
Best Local Similarity 53.2%; Pred. No. 2.4e-64;
Matches 117; Conservative 31; Mismatches 62; Indels 10; Gaps 4;

QY 6 SLSSVSRTFTVAPAAFI--RAKHTLPPLPAYDALEPSISKEIMTLHHTKHQTYVNGL 63
DB 5 AVCGTSRQ--LAPALGYLSRQKHSPLDIPYDGALEPHINAQIMQLHSHKHAAYVNNL 62
QY 64 NAAESYSAAVKGEDVLTQVKLSALKFNGGGHINHSIPWKNLAPYGSSEATLSGGLKK 123
DB 63 NVTEEKYQBALAKGDVTAQIALQPAKFKNGGGHINHSIPWNLSPNGGGE---PKGELLE 119
QY 124 AIEESFGSFEAPKKFNADTAAVQSGWGLGNPLTKKLEVTITANODPL---LTHIPI 180
DB 120 AIKRDGSGDFKFEKLTAAVQSGWGLGNPKKRAHLQIAACPNNDPLQGTGLIPL 179
QY 181 IGVDTWEHAFYLYQKNRPDYLAADVMSVINYKEAEARLQA 220
DB 180 LGIDVWEHAYLYQKNRPDYLAADVMSVINYKEAEARLQA 219

RESULT 8
US-08-880-342-28
Sequence 28, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-880-342-28

Query Match 53.6%; Score 618; DB 3; Length 222;
Best Local Similarity 53.6%; Pred. No. 2.4e-64;
Matches 118; Conservative 31; Mismatches 61; Indels 10; Gaps 4;

QY 6 SLSSVSROTFVAPAAFI--RAKHTLPELPYADALEPSISKIMTLHTKHCHQTYVNGL 63
Db 5 AVCGTSRQ--LAPALGYSRQRKHSUPDLPDYGALEPHINAQIMQLHSHKHAAYVNNL 62

QY 64 NAAEESYSAAGKEDVLTQVKSALKFNGGGHINSLFWKNLAPYGSSEATLSEGLPKK 123
Db 63 NVNEEYQOEALAKGDVTAQALQALPKFNGGGHINSHIFWNLSPNGGGE---PKGELLE 119

QY 124 AIESFGSFEAFKKFNADTAAGVSGGWGLNPLTKLEVTITANQDPL---LTHIPI 180
Db 120 AIKRDFSGDFKFEKLTAAASVGVSGGWGLNPKERGHQIAACPNQDPLQGTGTGLIPL 179

QY 181 IGVDIWEHAFYLOKKNPKDYLAAVSVINYNKEAEARLQA 220
Db 180 LGIDVWEHAYILOKKNRPDYLKAIWNVINWNTERYMA 219

RESULT 9
US-08-023-980B-44
Sequence 44, Application US/08023980B
Patent No. 5843641
GENERAL INFORMATION:
APPLICANT: Brown, Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 585 Commercial Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-1024
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/023,980B
FILING DATE: 26-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/177001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/723-4123
TELEFAX: 617/723-8962
TELEX:
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-023-980B-44

Query Match 53.5%; Score 617; DB 2; Length 222;
Best Local Similarity 53.6%; Pred. No. 3.2e-64;
Matches 118; Conservative 30; Mismatches 62; Indels 10; Gaps 4;

QY 6 SLSSVSROTFVAPAAFI--RAKHTLPELPYADALEPSISKIMTLHTKHCHQTYVNGL 63
Db 5 AVCGTSRQ--LAPALGYSRQRKHSUPDLPDYGALEPHINAQIMQLHSHKHAAYVNNL 62

QY 64 NAAEESYSAAGKEDVLTQVKSALKFNGGGHINSLFWKNLAPYGSSEATLSEGLPKK 123
Db 63 NVNEEYQOEALAKGDVTAQALQALPKFNGGGHINSHIFWNLSPNGGGE---PKGELLE 119

QY 124 AIESFGSFEAFKKFNADTAAGVSGGWGLNPLTKLEVTITANQDPL---LTHIPI 180
Db 120 AIKRDFSGDFKFEKLTAAASVGVSGGWGLNPKERGHQIAACPNQDPLQGTGTGLIPL 179

QY 181 IGVDIWEHAFYLOKKNPKDYLAAVSVINYNKEAEARLQA 220
Db 180 LGIDVWEHAYILOKKNRPDYLKAIWNVINWNTERYMA 219

RESULT 10
US-08-486-953A-52
Sequence 52, Application US/08486953A
Patent No. 5849290
GENERAL INFORMATION:
APPLICANT: Brown, Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,953A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,052
FILING DATE: 28-FEB-1994
ATTORNEY/AGENT INFORMATION:

Query Match	53.5%	Score 617	DB 3	Length 222
Best Local Similarity	53.6%	Pred. No. 3.2e-64		
Matches 118	Conservative	30	Mismatches 62	Indels 10
Gaps				
Qy	6	SLSVSRQTEVAPAAFOI--RAKHTTPELPYAYDALEPSISKEIMTLHHTKHHQTYVNGL	63	
Db	5	AVCCTSFQ--LAPALGYLGSRKQSLPDPDYGALEPHINAQIMQLHSHKHAAYVNNL	62	
Qy	64	NAAEESYSAVGHGEDVLTVKLSALKFNGGGGHINHSLFWKNLAPYGSBATLSEGLPKK	123	
Db	63	NVTEEKYQEAALAGDVTAAQTALPALKFNGGGGHINHSIFWTNLSFNGGGE--PKGELLE	119	
Qy	124	AIESFGSPFAFKKFNADTAAVQSGSGWGLGNPLTKLEVTVTANQDPL---LTHIPI	180	
Db	120	AIKRDGSGFKFEKLTAAVSGVQSGSGWGLGPNKERGHQIAACPNQDPLQGTGLIPL	179	
Qy	181	IGVDIWEHAFYLOYNKVPDYLAAVWSVINYKEAEARLQA	220	
Db	180	LGDVMEWHAYLOYKNRPDYLKAIWVNWENVTERYMA	219	

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RESULT 12
5240847-10
;Patent No. 5240847
;APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
;ZOPHEL, ANDREAS; KRYSTEK, EDELTRAUD; MAURER-FOGY, INGRID;
;WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
;TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
;(HMN-SOD)
;NUMBER OF SEQUENCES: 34
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/167,261
;FILING DATE: 11-MAR-1988
;SEQ ID NO:10:
;LENGTH: 198
5240847-10

Query Match          52.9%; Score 610; DB 6; Length 198;
Best Local Similarity 56.1%; Pred. No. 1.8e-63;
Matches 111; Conservative 27; Mismatches 54; Indels 6; Gaps 2;

Qy      26   KHTLPETPYAYDALPESISKEINTLHHTKKHQTTVYGLNAAEISYSAAVGEDVLTQVKL 85
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Db      1   KHSLPDLPDYDGALEPHINAQIMQLHHSKHAAAYVNMLNVTEEKYQEALAKGDVTTAQAL 60

Qy      86   QSALKFKNGGHHINSHLFWKNLAIPVGSBEATLSSEGPLKKAIBESTFGSFEAFKKFNADTAA 145
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Db      61   QPALKFNGGGHHINSIFWNLSPPNGGE---PKGELLEAIKRDFSGDPFKKELTAASVG 117

Qy      146  VQSGGWGLGNPLTKKLEVTTTANQDPL---LTHPIPIGVDIWEHAFYLOYKNVKPDYL 202
       |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      118  VQSGGWGLGFNGKERGHGLQIAACFNQDPLQGTGTLIPLLIGIDVMEHAYLOYKNVRPDL 177

Qy      203  AAWWSVINYEAEARLOA 220
       |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,019
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2848-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-075-019-7

Query Match 52.6%; Score 607; DB 3; Length 226;
Best Local Similarity 56.1%; Pred. No. 4.9e-63;
Matches 111; Conservative 26; Mismatches 55; Indels 6; Gaps 2

Qy 26 KHTLPPLPYADALEPSISKEIMTLHTKHQTYVNGLNAAESYSAAVGKEDVLTQVKL 85
Db 3 KHSILPDPYDGALEPHINAQIMQLHSHKHAAYVNNLVNTEEKYQALAKGDVTAQTAL 62

Qy 86 QSALKKNGGGHHNHSLEFWKNLAPVGSSEATLSEGPLKKAIBESFGSPEAPFKKFNADTAA 145
Db 63 QPALKKNGGGHHNHSIFWNLSPNGGE---PKGELLEAIKRDGFSDFKPKKLTAAASVG 119

Qy 146 VQSGSGWLGILNPLTKKLEVTITTAQNPQL--LTHPIPLIGVDIWEHAFYLYQKNVKPDYL 202
Db 120 VQSGSGWLGFGNERGHLOIAACPNDPLOGTGLIPLIGDIDWEHAFYLYQKNVRPDYL 179

Qy 203 AAVSVNVYKAEARLQA 220
Db 180 KAIWNVINWENVTRYMA 197

RESULT 15
5240847-11
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRYSYK, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASAPAN, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1988
; SEQ ID NO: 11:
; LENGTH: 198
5240847-11

Query Match 52.6%; Score 606; DB 6; Length 198;
Best Local Similarity 55.8%; Pred. No. 5.2e-63;
Matches 110; Conservative 28; Mismatches 54; Indels 6; Gaps 2

Qy 26 KHTLPPLPYADALEPSISKEIMTLHTKHQTYVNGLNAAESYSAAVGKEDVLTQVKL 85

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Db	61	QPALKFNGGGHINHSIFWTNLSPNGGE---PKGELLEAIKRDFGSPDKFKEKLTAAASVG	117
Qy	146	VQSGSGWGLNPLTKKLEVTTTANQDPL--LTHIPIIGVDIWEHAFYLOYKNVKPDYL	202
Db	118	VQSGSGWGLGENKERGHLQIAACPNQDPLQGTGTLPLLGIDVWEHAYYLOYKNVRPDL	177
Qy	203	AAVWSVINYKEAEARLQA	220
Db	178	KAIWNVINWENVTERYMA	195

Search completed: March 30, 2004, 17:13:41
Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2004, 17:09:18 ; Search time 42 Seconds
(without alignments)
1383.070 Million cell updates/sec

Title: US-09-727-855B-5

Perfect score: 1153

Sequence: 1 MSVRASLSVSRQTFVAPAA.....AAVWSVINYKEARLQAL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1065169 seqs, 261661801 residues

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*

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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*

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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*

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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1153	100.0	222	9 US-09-727-855B-5	Sequence 5, Appli
2	748.5	64.9	200	14 US-10-230-331-27	Sequence 27, Appl
3	741.5	64.3	198	9 US-09-727-855B-7	Sequence 7, Appli
4	692	60.0	224	14 US-10-109-670-11	Sequence 11, Appl
5	668.5	58.0	206	14 US-10-109-670-10	Sequence 10, Appl
6	634.5	55.0	222	14 US-10-230-331-22	Sequence 22, Appl
7	629.5	54.6	222	14 US-10-230-331-20	Sequence 20, Appl
8	618	53.6	222	14 US-10-230-331-19	Sequence 19, Appl
9	603.5	52.3	240	12 US-10-424-599-233245	Sequence 233245,
10	602.5	52.3	241	12 US-10-424-599-233247	Sequence 233247,
11	592	51.3	202	14 US-10-230-331-21	Sequence 21, Appl
12	589	51.1	233	15 US-10-310-154-662	Sequence 662, App
13	586	50.5	235	14 US-10-230-331-26	Sequence 26, Appl
14	582	50.5	228	14 US-10-230-331-25	Sequence 25, Appl
15	556.5	48.3	233	14 US-10-230-331-24	Sequence 24, Appl

16	513.5	44.5	214	15 US-10-289-762-75	Sequence 75, Appl
17	502	43.5	887	14 US-10-130-973A-6	Sequence 6, Appli
18	502	43.5	907	14 US-10-130-973A-5	Sequence 5, Appli
19	495	42.9	685	14 US-10-130-973A-7	Sequence 7, Appli
20	495	42.9	862	14 US-10-130-973A-4	Sequence 4, Appli
21	495	42.9	882	14 US-10-130-973A-3	Sequence 3, Appli
22	479	41.5	200	9 US-09-818-564-2	Sequence 2, Appli
23	479	41.5	200	9 US-09-738-626-6727	Sequence 6727, App
24	462	40.1	233	14 US-10-230-331-28	Sequence 28, Appl
25	430.5	37.3	188	9 US-09-987-190-6	Sequence 12947, A
26	414	35.9	213	14 US-10-156-761-12947	Sequence 23, Appl
27	339.5	29.4	193	14 US-10-230-331-23	Sequence 663, App
28	339.5	29.4	193	15 US-10-310-154-663	Sequence 664, App
29	334	29.0	201	15 US-10-310-154-664	Sequence 7867, App
30	327.5	28.4	213	12 US-10-335-977-7867	Sequence 7868, App
31	327.5	28.4	218	12 US-10-335-977-7868	Sequence 59803, A
32	309.5	26.8	257	12 US-10-425-114-59803	Sequence 16, Appl
33	305	26.5	191	14 US-10-230-331-16	Sequence 29, Appl
34	305	26.5	191	14 US-10-230-331-29	Sequence 244384,
35	300	26.0	293	12 US-10-424-599-244384	Sequence 279326,
36	290	25.2	284	12 US-10-424-599-279326	Sequence 6, Appli
37	258	22.4	386	12 US-10-425-114-59796	Sequence 59796, A
38	255	22.1	95	9 US-09-993-333-12	Sequence 12, Appl
39	246	21.3	171	12 US-10-424-599-188362	Sequence 188362,
40	232	20.1	169	12 US-10-424-599-233242	Sequence 233242,
41	227.5	19.7	175	12 US-10-425-114-70586	Sequence 70586, A
42	222	19.3	225	12 US-10-425-114-59797	Sequence 59797, A
43	195.5	17.0	311	12 US-10-425-114-59795	Sequence 59795, A
44	191	16.6	240	12 US-10-425-114-59794	Sequence 59794, A
45	190.5	16.5	218	12 US-10-425-114-59362	Sequence 59362, A

ALIGNMENTS

RESULT 1

US-09-727-855B-5

; Sequence 5, Application US/09727855B

; Patent No. US20020168703A1

; GENERAL INFORMATION:

; APPLICANT: HOSHINO, Tatsuo

; APPLICANT: OJIMA, Kazuyuki

; APPLICANT: SITOUCUCHI, Yutaka

; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL

; TITLE OF INVENTION: MATERIALS THEREOF

; FILE REFERENCE: C38435/111694

; CURRENT APPLICATION NUMBER: US/09/727,855B

; FILING DATE: 2000-12-01

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 5

; LENGTH: 222

; TYPE: PRT

; ORGANISM: Phaffia rhodozyma

US-09-727-855B-5

Query Match	100.0%;	Score 1153;	DB 9;	Length 222;
Best Local Similarity	100.0%;	Pred. No. 4e-114;		
Matches 222;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MSVRASLSVSRQTFVAPAA	QIARAKHTIPELPYADALEPSISKEIMTLHHTKHQTYV	60
Db	1	MSVRASLSVSRQTFVAPAA	QIARAKHTIPELPYADALEPSISKEIMTLHHTKHQTYV	60
QY	61	NGLNAAEESYSAVGGKEDVLTQVKLSALKFNGGGGHNSLFWKNLAPYGESEATLSEGP	120	
Db	61	NGLNAAEESYSAVGGKEDVLTQVKLSALKFNGGGGHNSLFWKNLAPYGESEATLSEGP	120	
QY	121	LKKAIBESFGSFEAFKKKFNADTAQVQSGWGLGNPLTKKLEVTTTANQDPLLLTHIPI	180	
Db	121	LKKAIBESFGSFEAFKKKFNADTAQVQSGWGLGNPLTKKLEVTTTANQDPLLLTHIPI	180	
QY	181	IGVDIWEHAFYIQKNVKPDYLAAMVSNVINYKEARLQAL	222	

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Db 181 IGVDIWEHAFYQYKKNVDPYLAADVSVINKEAEARLQAAL 222
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RESULT 2
US-10-230-331-27
; Sequence 27, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 27
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ganoderma microsporum
US-10-230-331-27
Query Match 64.9%; Score 748.5; DB 14; Length 200;
Best Local Similarity 71.6%; Pred. No. 3.6e-71;
Matches 141; Conservative 24; Mismatches 23; Indels 9; Gaps 3;
Qy 27 HTLPDPYDALPESISKEIMTLHHTKHOTYVNGLNAAESYS-AAVGKEDVLTQVKL 85
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Db 3 HVLDPDPYVNALEPFISQIMELHKKHHTQYVNSLNAAEQAVAKASTPKX-RIAL 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 86 QSALKFNGGGHINSLFWKNLAPYGSB---EATLSEGLKKAIEESFGSPFAEAPKKKENA 141
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 QSALKFNGGGHINSLFWKNLAPAKSEKGGKGGALADGLPKSALEQNWGSVDNFIKEFNA 118
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 142 DTAAVQSGGWGLGNPLTKKLEVTITANQDPLTHIPIIGVDIWEHAFYQYKKNVDPY 201
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 TTAALQSGGWGLGNLPATKRELEITITANQDPLSHVPIIGVDIWEHAFYQYKKNVDPY 178
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 202 LAADVSVINKEAEARL 218
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 179 LAADIWIVINFEAEERL 195
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 3
US-09-727-855B-7
; Sequence 7, Application US/09727855B
; Patent No. US20020168703A1
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; APPLICANT: SETOGUCHI, Yutaka
; TITLE OF INVENTION: PROCESS FOR THE MANUFACTURE OF CAROTENOIDS AND BIOLOGICALLY USEFUL
; FILE REFERENCE: C38435/111694
; CURRENT APPLICATION NUMBER: US/09/727,855B
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Phaffia rhodozyma
US-09-727-855B-7
Query Match 64.3%; Score 741.5; DB 9; Length 198;
Best Local Similarity 69.7%; Pred. No. 2e-70;
Matches 138; Conservative 20; Mismatches 37; Indels 3; Gaps 1;
Qy 25 AKHLPELPYDALPESISKEIMTLHHTKHOTYVNGLNAAESYSAAVGKEDVLTQVK 84
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 APTLPELPYDALPEYISKEIMTLHHSKHHQTYVTNLNAAIQAFSQT---NDIKAQIA 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
Qy 85 QSALKFNGGGHINSLFWKNLAPYGSSEATLSEGLKKAIEESFGSPFAEAPKKKFNADTA 144
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Db 59 QSALKFNGGGHINSLFWKNMAPADSADAKLTGSLKTAIDKDFGSEFEKFKFNATL 118
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 145 AVQSGGWGLGNPLTKKLEVTITANQDPLTHIPIIGVDIWEHAFYQYKKNVDPYLA 204
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 GVQSGGWGLGYNTATKHLIATITANQDPLTLTPIIGLDIWEHAFYQYKKNVDPYLA 178
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 205 VMSVINKEAEARLQAAL 222
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 179 FMYVCFNAEQRREDAV 196
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 4

```
US-10-109-670-11
; Sequence 11, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 11
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Malassezia furfur
US-10-109-670-11
Query Match 60.0%; Score 692; DB 14; Length 224;
Best Local Similarity 59.3%; Pred. No. 4.4e-65;
Matches 128; Conservative 31; Mismatches 53; Indels 4; Gaps 1;
Qy 11 SRQTFVAP----AAPQTRAKHTLPDPYDALPESISKEIMTLHHTKHOTYVNGLNAA 66
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 TRRAAAPLANAAQMGVTKYTLPLPYDYGALPEAISGEIMETHYKHHRTYVNNLNA 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 67 EESYSAVKGEDVLTQVKLSALKFNGGGHINSLFWKNLAPYGSSEATLSEGLKKAIE 126
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 EDKLIDALPQSPGLGEITAEALNAIFNGGGHINSLFWKNLAPTKNGGELDSGEURSAID 125
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 127 ESFGSFEAFKKKFNADTAAVQSGGWGLGNPLTKKLEVTITANQDPLTHIPIIGVDI 186
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 126 RDFSVDAMKEKFNALAGIQSGGWGLGNLTQKLDIITANQDPLSHKPLIGIDAM 185
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 187 EHAFYQYKKNVDPYLAADVSVINKEAEARLQAAL 222
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 186 EHAFYQYKKNVADYFKAIWTVINFEAEKRLKEAL 221
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 5

```
US-10-109-670-10
; Sequence 10, Application US/10109670
; Publication No. US20030105283A1
; GENERAL INFORMATION:
; APPLICANT: TAKESAKO, KAZUTOH et al.
; TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN MALASSEZIA
; FILE REFERENCE: 1422-0523P
; CURRENT APPLICATION NUMBER: US/10/109,670
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 10
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Malassezia furfur
US-10-109-670-10
Query Match 58.0%; Score 668.5; DB 14; Length 206;
Best Local Similarity 63.1%; Pred. No. 1.2e-62;
Matches 123; Conservative 24; Mismatches 47; Indels 1; Gaps 1;
```



```

QY 23 IRAKHTLPPLPYAYDALEPSISKEIMTLHHTKHQTYVGNLAAEESYSAVGVKEDVLQ 82
Db 3 VMEYTLPLPLPYAYDALEPSISKEIMTVHDKHQTIVNNLNAEAKAYABATAANDVLQ 62

QY 83 VKLOSALKFNGGGHINHSFWKNLAPYGSSEATLSEGPLKKAIESFGSFEAFKKFNAD 142
Db 63 IQQSALKFNGGGHINHSFWKNLAPYGSSEATLSEGPLKKAIESFGSFEAFKKFNAD 122

QY 143 TAAVQSGGWLGLNPLTKKLEVTTTANQDPLTHPIIGVDIWEHAFYLYQKNVDPYL 202
Db 123 AAGIQSGWLGLVAP-TGNLDLVVAKDQDPLTHPIIGVDIWEHAFYLYQKNVDPYL 202

QY 203 AAVSVVINYKEAEAR 217
Db 182 KAWNVVNWAEAEKR 196

RESULT 6
US-10-230-331-22
; Sequence 22, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 22
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-230-331-22

Query Match
Best Local Similarity 55.0%; Score 634.5; DB 14; Length 222;
Matches 123; Conservative 30; Mismatches 58; Indels 11; Gaps 4;

QY 1 MSVRASLSVSRQTFVAPAAFOI--RAKHTLPPLPYAYDALEPSISKEIMTLHHTKHQ 58
Db 1 MLCRAACASGR---LGPAASTAGSRKHSLPDPYDYGALPHINAQIMQLHSHKHAT 57

QY 59 YVGNLAAEESYSAVGVKEDVLTVKLSALKFNGGGHINHSFWKNLAPYGSSEATLSE 118
Db 58 YVNNLVNTEKYEALAKGDVTTQVALQPAKFGGGHINHSIFWNLSPKGGGE---PK 114

QY 119 GPLKKAIESFGSFEAFKKFNADTAAVQSGGWLGLNPLTKKLEVTTTANQDPL---L 175
Db 115 GELLEAIKRDGFSFEKFEKLTAVSVGVQSGGWLGFNKEQGRLOIAACSNQDPLQGT 174

QY 176 THPIIGVDIWEHAFYLYQKNVDPYLAAVSVINYKEAEAR 217
Db 175 GLTILGIDWEHAYLYQKNVRPDKALWNVINWENVSQR 216

RESULT 7
US-10-230-331-20
; Sequence 20, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 20

```

```

; LENGTH: 222
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-230-331-20

Query Match
Best Local Similarity 54.6%; Score 629.5; DB 14; Length 222;
Matches 121; Conservative 32; Mismatches 63; Indels 7; Gaps 3;

QY 1 MSVRASLSVSRQTFVAPAAFOI--RAKHTLPPLPYAYDALEPSISKEIMTLHHTKHQ 60
Db 1 MLSRAACST--SRLVLPALSVLGRQKHSPLDPYDYGALPHINAQIMQLHSHKHAAYV 59

QY 61 NGLNAAEESYSAVGVKEDVLTVKLSALKFNGGGHINHSFWKNLAPYGSSEATLSEGP 120
Db 60 NNUNVAEKEYREALEKGDVTAQIALQPAKFGGGHINHSIFWNLSPKGGGE---PQ 116

QY 121 LKKAIESFGSFEAFKKFNADTAAVQSGGWLGLNPLTKKLEVTTTANQDPL---LTH 177
Db 117 LLEAIKRDGFSFEKFEKLTAVSVGVQSGGWLGFNKEQGRLOIAACSNQDPLQGT 176

QY 178 IPIIGVDIWEHAFYLYQKNVDPYLAAVSVINYKEAEARLQA 220
Db 177 IPLLIGIDWEHAYLYQKNVRPDKALWNVINWENVTARYTA 219

RESULT 8
US-10-230-331-19
; Sequence 19, Application US/10230331
; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 19
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-331-19

Query Match
Best Local Similarity 53.6%; Score 618; DB 14; Length 222;
Matches 115; Conservative 30; Mismatches 67; Indels 6; Gaps 2;

QY 6 SLSSVSRQTFVAPAAFOI--RAKHTLPPLPYAYDALEPSISKEIMTLHHTKHQTYVGN 65
Db 5 AVCGTSRQALAPALGVLSGRQKHSPLDPYDYGALPHINAQIMQLHSHKHAAYVNNLV 64

QY 66 ABEESYSAVGVKEDVLTVKLSALKFNGGGHINHSFWKNLAPYGSSEATLSEGPLKKA 125
Db 65 TEEKYQBALAKGDVTAQIALQPAKFGGGHINHSIFWNLSPKGGGE---PKGELLEAI 121

QY 126 EESFGSFEAFKKFNADTAAVQSGGWLGLNPLTKKLEVTTTANQDPL---LTHPIIG 182
Db 122 KRDFGSDKFEKLTAAASVGVQSGGWLGFNKEQGRLOIAACSNQDPLQGTGLIPILG 181

QY 183 VDIWEHAFYLYQKNVDPYLAAVSVINYKEAEARLQA 220
Db 182 IDWWEHAYLYQKNVRPDKALWNVINWENVTARYMA 219

RESULT 9
US-10-424-599-233245
; Sequence 233245, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

```



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; Publication No. US20030157513A1
; GENERAL INFORMATION:
; APPLICANT: RAJASEKHARAN, Ram
; TITLE OF INVENTION: A NOVEL TRIACYLGLYCEROL BIOSYNTHESIS IN THE CYTOSOL OF EUKARYOTES
; FILE REFERENCE: 110522
; CURRENT APPLICATION NUMBER: US/10/230,331
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/315,757
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 233
; TYPE: ERT
; ORGANISM: Pisum sativum
; US-10-230-331-24

Query Match      48.3%; Score 556.5; DB 14; Length 233;
Best Local Similarity 52.6%; Pred. No. 1.2e-50;
Matches 121; Conservative 28; Mismatches 48; Indels 33; Gaps 8;

Qy  4 RASLSSVSQRQ-----TFVAPAAQIRAKH--TLPELPYAYDALEPSISKEIMTLIHHTKH 55
Db  9 RKTLSVLNDAXPIGAAIAAASTQSRGLHVFTLPDLAYDYGALEPVISGEIMQIHOKH 68
Qy  56 HOTVYNGLNAAEESYSAAGKEDVLTQVKLOSALKFNGGGHINHSIFWKNLAPYGSEAT 115
Db  69 HQTITNKNKALEQLHDVAKADTSTTVKLNQAIKFNNGGGHINHSIFWKNLAP----- 121
Qy  116 LSEG---PLKK---AIEESFGSFEAFKKFNADTAAVOGSGWGLNPLTKKLEVT 168
Db  122 VSEGGEPPRESIGWAIIDTFGSLLEALIQKINAEGAALQ-----WGLDKOLKRLVWETT 176
Qy  169 ANQDPLLTH----IPICVDIWEHAFYLOYKNVKPDYLAADVSVINYKEA 214
Db  177 --QDPLVTKGASLVPELLGIDWEHAYLYQKNVREDYLNKINWKVINWKHA 224

Search completed: March 30, 2004, 17:11:53
Job time : 43 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2004, 17:09:18 ; Search time 45 seconds
(without alignments)
1556.556 Million cell updates/sec

Title: US-09-727-855B-5

Perfect score: 1153

Sequence: 1 MSVRSLSSVSRTQTFVAPAA.....AAVMSVINYKEAEARLQAAL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

1: sp.archaea.*

2: sp.bacteria.*

3: sp.fungi.*

4: sp.human.*

5: sp.invertebrate.*

6: sp.mammal.*

7: sp.mhc.*

8: sp.organelle.*

9: sp.phage.*

10: sp.plant.*

11: sp.podent.*

12: sp.virus.*

13: sp.vertebrate.*

14: sp.unclassified.*

15: sp.rviro.*

16: sp.bacteriap.*

17: sp.archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	751.5	65.2	206	3 Q96W28	Q96W28 phanerochaete
2	739.5	64.1	206	3 Q97773	Q97773 paxillus in
3	644.5	55.9	224	13 Q90Y34	Q90Y34 gallus gall
4	643.5	55.8	224	13 Q9DDJ1	Q9DDJ1 gallus gall
5	637.5	55.3	224	13 Q802D9	Q802D9 melopsittac
6	625.5	54.2	218	5 Q9NB66	Q9NB66 callinectes
7	617	53.5	213	4 Q727M4	Q727M4 homo sapien
8	616	53.4	222	4 Q6EE66	Q6EE66 homo sapien
9	615	53.3	199	6 Q8HXP4	Q8HXP4 macaca fasc
10	615	53.3	199	6 Q8HXP3	Q8HXP3 macaca fasc
11	615	53.3	199	6 Q8HXP2	Q8HXP2 macaca mulla
12	614	53.3	210	4 Q727M6	Q727M6 homo sapien
13	614	53.3	218	5 Q7YXMS	Q7YXMS apis mellif
14	614	53.3	231	10 Q65324	Q65324 raphanus sa
15	612.5	53.1	237	10 Q9M532	Q9M532 euphorbia e
16	611	53.0	199	6 Q8HXP5	Q8HXP5 hylobates l

17	610	52.9	199	6 Q8HXP7	Q8HXP7 pan troglod
18	610	52.9	199	6 Q8HXP6	Q8HXP6 pongo pygma
19	608	52.7	213	4 Q7Z7M7	Q7Z7M7 homo sapien
20	608	52.7	231	10 Q947R3	Q947R3 raphanus sa
21	607	52.6	209	4 Q7Z7M5	Q7Z7M5 homo sapien
22	606	52.6	231	10 Q8LEP0	Q8LEP0 arabidopsis
23	605	52.5	199	6 Q8HXP1	Q8HXP1 cebus apell
24	605	52.5	199	6 Q8HXP0	Q8HXP0 callithrix
25	604	52.4	220	5 Q8MUI6	Q8MUI6 trichinella
26	600	52.0	228	10 Q9SNM64	Q9SNM64 prunus pers
27	598	51.9	237	3 Q873M4	Q873M4 malassezia
28	596.5	51.7	224	10 Q9FY33	Q9FY33 digitalis l
29	596	51.7	226	10 Q84V26	Q84V26 avicennia m
30	595	51.7	231	10 Q96185	Q96185 triticum ae
31	590.5	51.2	231	10 Q43121	Q43121 oryza sativ
32	590.5	51.2	231	10 Q43803	Q43803 oryza sativ
33	587	50.9	231	10 P93606	P93606 triticum ae
34	584	50.7	235	10 Q43273	Q43273 zea mays m
35	581	50.4	205	10 Q9STB5	Q9STB5 hevea bras
36	581	50.4	205	10 Q9FSJ2	Q9FSJ2 hevea bras
37	574	49.8	234	10 Q84W70	Q84W70 arabidopsis
38	574	49.8	240	10 Q82584	Q82584 zantedesch
39	574	49.8	241	10 Q9LYK8	Q9LYK8 arabidopsis
40	571.5	49.6	216	10 Q9FY32	Q9FY32 digitalis l
41	570.5	49.5	224	10 Q82571	Q82571 triticum ae
42	566.5	49.1	230	3 Q874B1	Q874B1 cordyceps m
43	565	49.0	207	3 Q877B6	Q877B6 aspergillus
44	556.5	48.3	142	3 Q92464	Q92464 ganoderma t
45	555.5	48.2	142	3 Q92425	Q92425 ganoderma l

ALIGNMENTS

RESULT 1

Q96W28	ID	Q96W28	PRELIMINARY;	PRT;	206 AA.
AC	Q96W28;				
DT	01-DEC-2001	(TREMREL. 19, Created)			
DT	01-DEC-2001	(TREMREL. 19, Last sequence update)			
DT	01-OCT-2003	(TREMREL. 25, Last annotation update)			
DE	Manganese superoxide dismutase (EC 1.15.1.1) (Superoxide dismutase (Mn/Fe)).				
DE	MNSOD1.				
OS	Phanerochaete chrysosporium.				
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;				
OC	Aphyllophorales; Corticiaceae; Phanerochaete.				
OX	NCBI_TaxID=5306;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BKM-F-1767;				
RA	Doresetz C.G., Goldberg D., Belinky P.A., Rothschild N., Krinfeld B., Kalati O., Burger M.;				
RT	"The manganese superoxide dismutase of Phanerochaete chrysosporium: its function, expression and gene structure."				
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.				
CC	-!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELL AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).				
CC	-!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2O(2)).				
CC	-!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.				
DR	EMBL;	AF388395;	AAK82369.1;	--	
DR	GO;	GO:0004785;	Fcopper, zinc superoxide dismutase activity;	IEA.	
DR	GO;	GO:0008382;	Firon superoxide dismutase activity;	IEA.	
DR	GO;	GO:0008383;	Fmanganese superoxide dismutase activity;	IEA.	
DR	GO;	GO:0046872;	Fmetal ion binding;	IEA.	
DR	GO;	GO:0016954;	Fnickel superoxide dismutase activity;	IEA.	
DR	GO;	GO:0014491;	Foxidoreductase activity;	IEA.	
DR	GO;	GO:0006801;	Fsuperoxide metabolism;	IEA.	
DR	InterPro;	IPR001189;	SODismutase.		
DR	Pfam;	PF00081;	sodfe.1.		
DR	Pfam;	PF02777;	sodfe.C.1.		
DR	PRINTS;	PR01703;	MNSODISMUTASE.		

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DR ProDom: PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase.
SQ SEQUENCE 206 AA; 22860 MW; 63625CCFBD44A290 CRC64;

Query Match 65.2%; Score 751.5; DB 3; Length 206;
Best Local Similarity 69.8%; Pred. No. 4.2e-60;
Matches 141; Conservative 25; Mismatches 27; Indels 9; Gaps 3;

QY 26 KHTLPPLPYADALEPSISKEIMTLHTKHQTVYVGNLNAAEESYS-AAVGKEDVLTVQVK 84
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 4 QHTLPDLPYADALEPYSQIIMTLHHKHHQTVVYVGNLNAAEESYSAAKTATPE---RIA 59
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 85 LQSALKFNGGGHINHSFWKNLAPVGSER---EATLSEGLPKKAIESFGSFEAFKKKFN 140
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 LQAALRENGGGHINHSFWKNLAPVGSER---EATLSEGLPKKAIESFGSFEAFKKKFN 119
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 141 ADTAAVQSGWGWLGNPLTKKLEVTITANODPLLTHPIIGVDIWEHAFYLYQKNVKPD 200
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 120 AATAAQSGWGWLGNPLTKKLEVTITANODPLLTHPIIGVDIWEHAFYLYQKNVKPD 179
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 201 YLAAVWSVINYKEAEARLQAL 222
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 180 YLNAINVINFKEAEKRTTEGL 201
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 3
Q90Y34
ID Q90Y34 PRELIMINARY; PRT; 224 AA.
AC Q90Y34;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MnSOD (EC 1.15.1.1) (Superoxide dismutase [Mn/Fel]).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim H., You S., Foster L.K., Farris J., Foster D.N.;
RT "Expression of antioxidant genes in primary and immortal chicken
   embryo fibroblast cells.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
   CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
   FAMILY.
CC EMBL; AF293988; AAK97214.1; -.
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
DR GO; GO:0008382; F:iron superoxide dismutase activity; IEA.
DR GO; GO:0008383; F:manganese superoxide dismutase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016954; F:nickel superoxide dismutase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe_C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase.
SQ SEQUENCE 224 AA; 24770 MW; A18570FC736BD3DD CRC64;

Query Match 55.9%; Score 644.5; DB 13; Length 224;
Best Local Similarity 54.9%; Pred. No. 2.4e-50;
Matches 123; Conservative 30; Mismatches 64; Indels 7; Gaps 3;

QY 1 MSVRASLSVSQRTFVAFAAFOI-RAKHTLPPLPYADALEPSISKEIMTLHTKHQTVY 59
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MLCRLASGRSRAALVAPLGLCVAKQHTLPDLPDYGALEPHISAEIMQLHSHKHAY 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 60 VGNLNAAEESYGAAGKEDVLTVQVKLQSALKFNGGGHINHSFWKNLAPVGSER---EATLSE 119
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 VNNLVNTEKYEALAKGVDVTAQVSLQPALKENGCGGHINHTILWTNLSFGSGGE---PKG 117
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 120 PLKKAIESFGSFEAFKKFNADTAAVQSGWGWLGNPLTKKLEVTITANODPLLTHPIIGVDI 176
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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Db 118 ELMEAIKRDGSGFANFEKLTAVSGVQSGWGLYNKEQGRQLQAACANQDPLQGTG 177
 QY 177 HIPLIGVDIWEHAFYLOYNKVPDYLAAYVMSVINYKEAEARLOA 220
 Db 178 LIPLIGDWEHAYFYLOYNKVRPDYLAIAWNVINWENASSRYES 221

RESULT 4

Q9DDJ1 PRELIMINARY; PRT; 224 AA.
 AC Q9DDJ1
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Manganese-containing superoxide dismutase precursor (EC 1.15.1.1)
 DE (Superoxide dismutase [Mn/Fel]).
 GN MNSOD.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Bu Y.O., Luo X.G., Li S.F., Lu C., Li Y.W., Kuang X., Liu B., Li J.F.,
 Yu S.X.;
 RT "Cloning and Sequence Analysis of Manganese-containing Superoxide
 Dismutase (MnSOD) cDNA of Chicken."
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 FAMILY.
 DR EMBL; AF323270; AAG46055.1; -.
 DR HSSP; P04179; IABM.
 DR GO; GO:0004785; F.copper, zinc superoxide dismutase activity; IEA.
 DR GO; GO:0008382; F.iron superoxide dismutase activity; IEA.
 DR GO; GO:0008383; F.manganese superoxide dismutase activity; IEA.
 DR GO; GO:0046872; F.metal ion binding; IEA.
 DR GO; GO:0016594; F.nickel superoxide dismutase activity; IEA.
 DR GO; GO:0016491; F.oxidoreductase activity; IEA.
 DR GO; GO:0006801; P.superoxide metabolism; IEA.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe; C; 1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD MN; 1.
 KW Oxidoreductase; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 224
 FT POTENTIAL.
 FT MANGANESE-CONTAINING SUPEROXIDE
 FT DISMUTASE.
 SQ SEQUENCE 224 AA; 24946 MW; 1192114C7266687F CRC64;

Query Match 55.8%; Score 643.5; DB 13; Length 224;
 Best Local Similarity 54.9%; Pred. No. 3e-50;
 Matches 123; Conservative 28; Mismatches 66; Indels 7; Gaps 3;
 QY 1 MSVRASLSVSRQTFVAP-AAFQIRAKHTLPPELAYDALEPSISKEIMTLHHTKHQTY 59
 Db 1 MLCRLASGRSAALVAPWGCLVARQKHTLPDYPYDYGALPHISAEIMQLHSHKHATY 60
 QY 60 VNLGNAEESYSAAGKEDVLTVKLSALKFNGGGHINHSFWKMLAPYGSSEATLSG 119
 Db 61 VNNLVNTEKYKEALAKGDVTAQVSLQPKLFNGGGHINHTIFWNLSPSGGE---PKG 117
 QY 120 PLKKAIEESFGFEAFKFFNADTAAVQSGWGLGNPLTKKLEVTITANODPL---IT 176
 Db 118 ELMEAIKRDGSGFANFEKLTAVSGVQSGWGLYNKEQGRQLQAACANQDPLQGTG 177

QY 177 HIPLIGVDIWEHAFYLOYNKVPDYLAAYVMSVINYKEAEARLOA 220
 Db 178 LIPLIGDWEHAYFYLOYNKVRPDYLAIAWNVINWENASSRYES 221

RESULT 5

Q802D9 PRELIMINARY; PRT; 224 AA.
 AC Q802D9
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Mn superoxide dismutase.
 GN SOD2.
 OS Melospittacus undulatus (Buderigar).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Psittaciformes; Psittacidae;
 OC Melospittacus.
 OX NCBI_TaxID=131146;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Austad S.N., Carlberg K.;
 RT "Melospittacus undulatus Mn superoxide dismutase (SOD2) gene."
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY241394; AAO72712.1; -.
 DR GO; GO:0046872; F.metal ion binding; IEA.
 DR GO; GO:0004784; F.superoxide dismutase activity; IEA.
 DR GO; GO:0006801; P.superoxide metabolism; IEA.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe; C; 1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD MN; 1.
 SQ SEQUENCE 224 AA; 24704 MW; F45DA30D58501D40 CRC64;

Query Match 55.3%; Score 637.5; DB 13; Length 224;
 Best Local Similarity 56.4%; Pred. No. 1e-49;
 Matches 124; Conservative 25; Mismatches 62; Indels 9; Gaps 4;
 QY 7 LSSVSRQT--FVAP-AAFQIRAKHTLPPELAYDALEPSISKEIMTLHHTKHQTYVNGL 63
 Db 5 LSSAGRSSVKKVAPVGLCLASQKHTLPDYPYDYGALPHISAEIMQLHSHKHATVNNL 64
 QY 64 NAAEESYSAAGKEDVLTVKLSALKFNGGGHINHSFWKMLAPYGSSEATLSGPKK 123
 Db 65 NVAEEKYKEALAKGDVTAQVSLQPKLFNGGGHINHTIFWNLSPNGGGE---PKGELMD 121
 QY 124 AJEESFGFEAFKFFNADTAAVQSGWGLGNPLTKKLEVTITANODPL---LTHIFI 180
 Db 122 AIKRDGSGFANFEKLTAVSVGVQSGWGLYNKEQGRQLQAACANQDPLQGTGLIPL 181
 QY 181 IGVDIWEHAFYLOYNKVPDYLAAYVMSVINYKEAEARLOA 220
 Db 182 LGIDWEHAYFYLOYNKVRPDYLAIAWNVINWENASSRYAA 221

RESULT 6

Q9NB66 PRELIMINARY; PRT; 218 AA.
 AC Q9NB66
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Mitochondrial manganese superoxide dismutase precursor (EC 1.15.1.1)
 DE (Superoxide dismutase [Mn/Fel]).
 OS Callinectes sapidus (Blue crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Callinectes.
 OX NCBI_TaxID=6763;
 RN [1]
 RP SEQUENCE FROM N.A.

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Query Match      53.5%; Score 617; DB 4; Length 213;
Best Local Similarity 53.9%; Pred No. 7e-48;
Matches 117; Conservative 31; Mismatches 59; Indels 10; Gaps 4;

QY      6  SLSSVSRQTETVAPAAFOI--RAKHTLPPELPYAYDALEPSISKEIMTLHHTKHGHTYVNGL 63
DB      1  AVCGTSRQ--LAPALGYLGRSKQHSLPDLFDYDYGALPEPHINAQIMQLHSHKHAAYVNNL 58

QY      64 NAAEESYSAVGVKEDVLITQVKSALKFNGGGHINHSLFWNKLAPYGSSEATLSEGPLKK 123
DB      59 NVTEEKYQEALAKGDVTAQIALQPAKFNGGGHINHSIFWTNLSPNGGGE---PKGELLE 115

QY      124 AIBESFGSEAPFKKFNADTAATAVQSGWGMLGNPLTKLEVTITTAQNQDPL---LTHPI 180
DB      116 AIKRDGSGFKFKELTAASVGVQSGWGMLGFNKRGRHQLIAACPNQDPLQGTGLIPL 175

QY      181 IGVDIWEHAYLYQXNVKPDYLAASVINYKAEAR 217
DB      176 LGIDVWEHAYLYQXNVKRPDYLAINNVINWENVTER 212

RESULT 8
Q96EE6 PRELIMINARY; PRT; 222 AA.
AC Q96EE6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (EC 1.15.1.1) (Superoxide dismutase [Mn/Fe])
DE (Superoxide dismutase 2, mitochondrial).
DE SOD2.
GN GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kainine N., Chen X., Rols A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT vector."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC -!- CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR EMBL; BC012423.1; AAH12423.1; -.
DR EMBL; AY267901; AAP03428.1; -.
DR EMBL; BT006967; AAP35613.1; -.
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
DR GO; GO:0008383; F:iron superoxide dismutase activity; IEA.
DR GO; GO:0046872; F:manganese superoxide dismutase activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016954; F:nickel superoxide dismutase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.

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DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Hypothetical protein; Oxidoreductase.
SQ SEQUENCE 222 AA; 24750 MW; CA047D7900AE5905 CRC64;

Query Match
  53.4%; Score 616; DB 4; Length 222;
Best Local Similarity 53.2%; Pred. No. 9.1e-48;
Matches 117; Conservative 31; Mismatches 62; Indels 10; Gaps 4;

QY 6 SLSSVSRTQFVAPAFQI--RAKHLPPLPYDALPSISKEIMTLHTKHQTYVNGL 63
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 5 AVCGTSRQ--LAPVLGSLGRKSHLPDLPYDYGALPHINAQIMQLHSHKHAAYVNNL 62
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 64 NAAEESYSAAVGKEDVLTQVLSALKFGNGGHHNLSFWKNLAPVGSSEATLSEGLPKK 123
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 63 NTEKYQELAKGVDTAQIALQPALKFGNGGHHNLSIFWTLNLSNGGGE---PKGELLE 119
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 124 AIEESFGFEAFKKFNADTAAVQSGGWLGLNPLTKKLEVTITANQDPL---LTHIP 180
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 AIKRDGFGDFKFKELTAASVGVQSGGWLGNKRGHQLIAACPNQDPLQGTGLIPL 179
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 181 IGVDIWEHAFYLYQKNVDDYLAADVWSVINYKEAEARLQA 220
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 180 LGIDWEHAYLYQKNVREDYLAAMNVINWENVTERYMA 219
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 9
QHXHP4 PRELIMINARY; PRT; 199 AA.
AC Q8HXP4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-WAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mn-superoxide dismutase.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22371545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RT superoxide dismutases.";
RL Gene 296:99-109 (2002).
DR EMBL; AB087277; BAC20356.1; -
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
SQ SEQUENCE 199 AA; 22340 MW; 43B9CBE138C7E563 CRC64;

Query Match
  53.3%; Score 615; DB 6; Length 199;
Best Local Similarity 56.6%; Pred. No. 9.6e-48;
Matches 112; Conservative 27; Mismatches 53; Indels 6; Gaps 2;

QY 26 KHTLPPLPYDALPSISKEIMTLHTKHQTYVNGLNAAEESYSAAVGKEDVLTQVKL 85
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 2 KHSPLDLPYDYGALPHINAQIMQLHSHKHAAYVNNLVNTEKYQELAKGVDTAQIAL 61
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 86 QSALKPNGGGHHNLSFWKNLAPVGSSEATLSEGLPKKAEESFGFEAFKKFNADTA 145
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 62 QPALKPNGGGHHNLSIFWTLNLSNGGGE---PKGELLEAIKRDGFGFEKFKELTA 118
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 146 VQSGGWLGLNPLTKKLEVTITANQDPL---LTHIPILGVDIWEHAFYLYQKNV 202
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 119 VQSGGWLGLGNKRGHQLIAACPNQDPLQGTGLIPLLGIDWEHAYLYQKNV 178
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 203 AAVWSVINYKEAEARLQA 220
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 179 KAIMNVINWENVTERYMA 196
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 11
QHXHP2 PRELIMINARY; PRT; 199 AA.
AC Q8HXP2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-WAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mn-superoxide dismutase.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
```

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DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Hypothetical protein; Oxidoreductase.
SQ SEQUENCE 222 AA; 24750 MW; CA047D7900AE5905 CRC64;

Query Match
  53.4%; Score 616; DB 4; Length 222;
Best Local Similarity 53.2%; Pred. No. 9.1e-48;
Matches 117; Conservative 31; Mismatches 62; Indels 10; Gaps 4;

QY 6 SLSSVSRTQFVAPAFQI--RAKHLPPLPYDALPSISKEIMTLHTKHQTYVNGL 63
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 5 AVCGTSRQ--LAPVLGSLGRKSHLPDLPYDYGALPHINAQIMQLHSHKHAAYVNNL 62
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 64 NAAEESYSAAVGKEDVLTQVLSALKFGNGGHHNLSFWKNLAPVGSSEATLSEGLPKK 123
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 63 NTEKYQELAKGVDTAQIALQPALKFGNGGHHNLSIFWTLNLSNGGGE---PKGELLE 119
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 124 AIEESFGFEAFKKFNADTAAVQSGGWLGLNPLTKKLEVTITANQDPL---LTHIP 180
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 120 AIKRDGFGDFKFKELTAASVGVQSGGWLGNKRGHQLIAACPNQDPLQGTGLIPL 179
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 181 IGVDIWEHAFYLYQKNVDDYLAADVWSVINYKEAEARLQA 220
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 180 LGIDWEHAYLYQKNVREDYLAAMNVINWENVTERYMA 219
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 9
QHXHP4 PRELIMINARY; PRT; 199 AA.
AC Q8HXP4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-WAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mn-superoxide dismutase.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22371545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RT superoxide dismutases.";
RL Gene 296:99-109 (2002).
DR EMBL; AB087277; BAC20356.1; -
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
SQ SEQUENCE 199 AA; 22340 MW; 43B9CBE138C7E563 CRC64;

Query Match
  53.3%; Score 615; DB 6; Length 199;
Best Local Similarity 56.6%; Pred. No. 9.6e-48;
Matches 112; Conservative 27; Mismatches 53; Indels 6; Gaps 2;

QY 26 KHTLPPLPYDALPSISKEIMTLHTKHQTYVNGLNAAEESYSAAVGKEDVLTQVKL 85
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 2 KHSPLDLPYDYGALPHINAQIMQLHSHKHAAYVNNLVNTEKYQELAKGVDTAQIAL 61
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 86 QSALKPNGGGHHNLSFWKNLAPVGSSEATLSEGLPKKAEESFGFEAFKKFNADTA 145
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 62 QPALKPNGGGHHNLSIFWTLNLSNGGGE---PKGELLEAIKRDGFGFEKFKELTA 118
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 146 VQSGGWLGLNPLTKKLEVTITANQDPL---LTHIPILGVDIWEHAFYLYQKNV 202
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 119 VQSGGWLGLGNKRGHQLIAACPNQDPLQGTGLIPLLGIDWEHAYLYQKNV 178
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 203 AAVWSVINYKEAEARLQA 220
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 179 KAIMNVINWENVTERYMA 196
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Teruka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RL superoxide dismutases."
RL Gene 296:99-109(2002).
DR EMBL; AB087279; BAC20358.1; -
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF02777; sodfe C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_NN; 1.
SQ SEQUENCE 139 AA; 23340 MW; 43B9CBE138C7E563 CRC64;

Query Match 53.3%; Score 615; DB 6; Length 199;
Best Local Similarity 56.6%; Pred. No. 9.6e-48;
Matches 112; Conservative 27; Mismatches 53; Indels 6; Gaps 2;

Qy 26 KHTLPPELAYDALEPSISKEIMTLHTKHHQTYVINGLNAAESYSAAVGKEDVLTQVKL 85
Db 2 KHSLEPDLFPDYGALEPHINAQIMQLHSHKHAAYVNNLNVTEKYQELAKGDTVTAQIAL 61
Qy 86 QSALKFNGGGHINHSFWKNLAPYGSSEATLSEGLKKAIESFGSFEAPKKFNADTAA 145
Db 62 QPALKFNGGGHINHSFWNLSNPGGE---PKGELLEAIKRDGSGFEKFEKLTAAASVG 118
Qy 146 VQSGSGWGLGNPLTKLEVTTTANQDPL---LTHPIIGVDIWEHAFYLOYNKVPDYL 202
Db 119 VQSGSGWGLGNPKRGQGLQIAACPNQDPLQGTGTLPLIGDVEHAYYLOYNKVPDYL 178
Qy 203 AAVWSVINYKEAEARLQA 220
Db 179 KAINNVINWENVTRYMA 196

RESULT 12
Q7Z7M6 PRELIMINARY; PRT; 210 AA.
AC Q7Z7M6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Manganese-containing superoxide dismutase (Fragment).
GN SOD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mukhopadhyay S., Das S.K., Mukherjee S.;
RT "Differential Expression of Mn-SOD Gene in Normal and Cancerous Human
RL Mammary Epithelial Cells."
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY280719; AAP34408.1; -
FT NON TER 1
FT NON TER 210
SQ SEQUENCE 210 AA; 23224 MW; 55B509814185894D CRC64;

Query Match 53.3%; Score 614; DB 4; Length 210;
Best Local Similarity 54.7%; Pred. No. 1.3e-47;
Matches 116; Conservative 31; Mismatches 55; Indels 10; Gaps 4;

Qy 6 SLSSVSQTFVAPAAFOI--RAKHTLPPELAYDALEPSISKEIMTLHTKHHQTYVNGL 63
Db 1 AVCQTSRQ--LAPALGYLGSQKSLPDLPYDYGALPHINAQIMQLHSHKHAAYVNNL 58
Qy 64 NAAESYSAAVGKEDVLTQVKLSALFKNGGGHINHSFWKNLAPYGSSEATLSEGLPK 123

Db 59 NVTEKYQELAKGDTVTAQIALQPALEKNGGGHINHSFWNLSNPGGE---PKGELLE 115
Qy 124 AIEESFGSFEAFKKFNADTAAVQSGSGWGLGNPLTKLEVTTTANQDPL---LTHPI 180
Db 116 AIKRDGSGFDKFEKLTAAVQSGSGWGLGNFKNGKHQIAACPNQDPLQGTGTLPL 175
Qy 181 IGVDIWEHAFYLOYNKVPDYLAAVWSVINYK 212
Db 176 LGIDVWEHAYYLOYNKVPDYLKAIWNVINWE 207

RESULT 13
Q7YXMS PRELIMINARY; PRT; 218 AA.
AC Q7YXMS;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mn superoxide dismutase (Fragment).
GN SOD2.
OS Apis mellifera ligustica (Common honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7469;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=21923762; PubMed=11932240;
RA Whitfield C.W., Band M.R., Bonaldo M.F., Kumar C.G., Liu L.,
RA Pardinas J.R., Robertson H.M., Soares M.B., Robinson G.E.;
RT "Annotated expressed sequence tags and cDNA microarrays for studies of
RT brain and behavior in the honey bee."
RL Genome Res. 12:555-566(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Corona M., Hughes K., Weaver D.B., Robinson G.E.;
RT "Longevity is not associated with high antioxidant gene expression in
RT honey bee queens."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY329356; AAP93582.1; -
FT NON TER 1
FT NON TER 218
SQ SEQUENCE 218 AA; 24567 MW; 6BB7ABBB599E7C7E CRC64;

Query Match 53.3%; Score 614; DB 5; Length 218;
Best Local Similarity 51.6%; Pred. No. 1.3e-47;
Matches 116; Conservative 33; Mismatches 62; Indels 14; Gaps 3;

Qy 1 MSVNASLSSVSQTFVAPAAFOIQAHTLPPELAYDALEPSISKEIMTLHTKHHQTYV 60
Db 3 VSYRILPSNTVKDTFT-----RTKHTLPDLPDYKALEPILSAEIMQLHSHKHAATYV 55
Qy 61 NGLNAAESYSAAVGKEDVLTQVKLSALFKNGGGHINHSFWKNLAPYGSSEATLSEGP 120
Db 56 NNLNVAEEKKVAAGDVNTQVALSPAIFKNGGGHINHSFWNLSNPGK-----PDAA 111
Qy 121 LKKAIBESFGSFEAFKKFNADTAAVQSGSGWGLGNPLTKLEVTTTANQDPLTH--- 177
Db 112 LLNQIKKDFGSIEMKKRLSENTIAIQSGSGWGLGYCQSKSLAIATCANQDPLQATTGL 171
Qy 178 IPTIGVDIWEHAFYLOYNKVPDYLAAVWSVINYKEAEARLQAAL 222
Db 172 IPLFGIDVWEHAYYLOYNKVPDYLKAIWNVINWVNSRYKKA 216

RESULT 14
O65324 PRELIMINARY; PRT; 231 AA.
ID O65324;
AC O65324;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Superoxide dismutase [Mn/Fe] (EC 1.15.1.1).
GN SOD.
```

OS *Raphanus sativus* (Radish).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Brassicales; Brassicaceae; Raphanus.
 OX NCBI_TaxID=3726;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kwon S.-I., An C.-S.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL; AF061333; AAC15806.1; -.
 DR PIR; T08181; T08181.
 DR HSSP; P04179; IQN9.
 DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
 DR GO; GO:0008382; F:iron superoxide dismutase activity; IEA.
 DR GO; GO:0008383; F:manganese superoxide dismutase activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0016954; F:nickel superoxide dismutase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006801; P:superoxide metabolism; IEA.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe_1.
 DR Pfam; PF02777; sodfe_C_1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 231 AA; 25353 MW; DD709E5DBFF81A80 CRC64;
 Query Match 53.3%; Score 614; DB 10; Length 231;
 Best Local Similarity 57.5%; Pred. No. 1.5e-47;
 Matches 122; Conservative 20; Mismatches 54; Indels 16; Gaps 2;
 QY 7 LSSVSRQTFVAPAAQIRAKHTLPPLPYADALEPSISKEIMTLHTKHOTYVNGLNAA 66
 Db 23 LGSRSIQTF-----TLPLPDYSALPAISGEIMQIHQKHQAYVTNNNA 70
 QY 67 EESYSAAGKEDVLTQVKLSALKFNGGGHINHSIFWKNLAPYGSBEATLSEGPLKKAIE 126
 Db 71 LEQLQAVNKGASAVVKLSAIFKNGGGHVNHSIFWKNLAPVKEGGEPKPSGLGAID 130
 QY 127 EESGFEAPKKFNADTAAGVQSGWGLGNPLTKKLEVTITANQDPLLTTH----IPIIG 182
 Db 131 TSFGSLEGLVKKMSAEGAAVQSGWVWLGIDKELKLVVDITANQDPLVTGKGLVPLVG 190
 QY 183 VDIWEHAFYLOYNKVPDYLAAVWSVINYKEA 214
 Db 191 IDVWEHAYLYQKNVRPDYLNKVNKVNKYA 222
 RESULT 15
 Q9M532 PRELIMINARY; PRT; 237 AA.
 AC Q9M532;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Manganese superoxide dismutase (EC 1.15.1.1) (Superoxide dismutase
 (Mn/Fel)).
 OS *Euphorbia esula* (Leafy spurge).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids I; Malpighiales; Euphorbiaceae; Euphorbioideae; Euphorbieae;
 CC *Euphorbia*.
 OX NCBI_TaxID=3993;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Underground adventitious buds;
 RA Anderson J.V., Horvath D.P.;

RT "Identification of mRNAs expressed in underground adventitious buds of
 RT *Euphorbia esula* (leafy spurge).";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR EMBL; AF242310; AAF65768.1; -.
 DR PIR; T50830; T50830.
 DR HSSP; P04179; IAP6.
 DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.
 DR GO; GO:0008382; F:iron superoxide dismutase activity; IEA.
 DR GO; GO:0008383; F:manganese superoxide dismutase activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0016954; F:nickel superoxide dismutase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006801; P:superoxide metabolism; IEA.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe_1.
 DR Pfam; PF02777; sodfe_C_1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD_MN; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 237 AA; 26215 MW; 87EE25907EB702E0 CRC64;
 Query Match 53.1%; Score 612.5; DB 10; Length 237;
 Best Local Similarity 56.3%; Pred. No. 2.1e-47;
 Matches 120; Conservative 25; Mismatches 63; Indels 5; Gaps 2;
 QY 7 LSSVSRQTFVAPAAQIRAKHT--LPELPYADALEPSISKEIMTLHTKHOTYVNGLN 64
 Db 14 LASNSAKLVSGSAVQLRGKFTFSLPDYDYGALPAISGEIMQIHQKHQHTITVYN 73
 QY 65 AAESYSAAVGKEDVLTQVKLSALKFNGGGHINHSIFWKNLAPYGSBEATLSEGPLKKA 124
 Db 74 KALEQLHEATEKGDSTTVVKLSAIFKNGGGHINHSIFWKNLAPVGGEGGELPHGSLGWA 133
 QY 125 IEESFGFEAPKKFNADTAAGVQSGWGLGNPLTKKLEVTITANQDPLLTTH---IPII 181
 Db 134 IDKDFGSLKLTQKNTQGAAGVQSGWVWLGLEKESKRLVWETTSNQDPLVTGKPLVPLV 193
 QY 182 GVDIWEHAFYLOYNKVPDYLAAVWSVINYKEA 214
 Db 194 GIDVWEHAYLYQKNVRPDYLNKVNKVNKYA 226
 Search completed: March 30, 2004, 17:10:21
 Job time : 48 secs

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OM protein - protein search, using sw model

Run on: March 30, 2004, 17:11:03 ; Search time 18 Seconds
(without alignments)
642.199 Million cell updates/sec

Title: US-09-727-855B-5
Perfect score: 1153
Sequence: 1 MSVRASLSVSQTTFVAPAA.....AAVWSVINYKEARLQAAL 222

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query % Match	Score	Length	ID	Description
1	748.5	64.9	200	1 SODM_GANMI	Q92429 ganoderma m
2	634.5	55.0	222	1 SODM_MOUSE	P09671 mus musculus
3	634.5	55.0	222	1 SODM_RAT	P07895 rattus norv
4	629.5	54.6	222	1 SODM_BOVIN	P41976 bos taurus
5	620	53.8	222	1 SODM_HUMAN	P04179 homo sapien
6	615.5	53.4	222	1 SODM_HORSE	Q9xs41 equus caball
7	615	53.3	198	1 SODM_MACFA	Q8hxp3 macaca fasc
8	615	53.3	198	1 SODM_MACFU	Q8hxp2 macaca mula
9	615	53.3	198	1 SODM_MACMU	Q8hxp4 macaca fusc
10	611	53.0	198	1 SODM_HYLLA	Q8hxp5 hyllobates l
11	610	52.9	198	1 SODM_PANTR	Q8hxp7 pan troglod
12	610	52.9	198	1 SODM_PONPY	Q8hxp6 pongo pygma
13	606	52.6	231	1 SODM_ARATH	O81235 arabidopsis
14	605	52.5	198	1 SODM_CALJA	Q8hxp0 callithrix
15	605	52.5	198	1 SODM_CBBAP	Q8hxp1 cebus apell
16	601	52.1	211	1 SODM_CAVPO	P49114 cavia porce
17	600	52.0	228	1 SODM_PRUPE	Q9sm64 prunus pers
18	595.5	51.6	217	1 SODM_DROME	Q00637 drosophila
19	595	51.6	233	1 SODM_HEVBR	P35017 hevea bras
20	592	51.3	202	1 SODM_RABIT	P41982 oryctolagus
21	592	51.3	228	1 SODM_NICPL	P11796 nicotiana p
22	590.5	51.2	231	1 SODM_ORYSA	Q43008 oryza sativ
23	590	51.2	233	1 SODP_MAIZE	P41980 zea mays (m
24	586	50.8	235	1 SODM_MAIZE	P09233 zea mays (m
25	584.5	50.7	221	1 SODM_CAEEL	P31161 caenorhabdi
26	583.5	50.6	210	1 SODM_ASFFU	Q92450 aspergillus
27	582	50.5	228	1 SODM_CAPAN	Q49066 capsicum an
28	572	49.6	218	1 SODN_CAEEL	P41977 caenorhabdi
29	570.5	49.5	232	1 SODN_MAIZE	P41978 zea mays (m
30	567.5	49.2	210	1 SODM_PENCH	O75000 penicillium
31	560	48.6	218	1 SODM_SCHPO	Q9uqx0 schizosacch
32	558	48.4	233	1 SODO_MAIZE	P41979 zea mays (m
33	556.5	48.3	233	1 SODM_PEA	P27084 pisum sativ

34	556.5	48.3	245	1 SODM_NEUCR	Q9y783 neurospora
35	555.5	48.2	200	1 SODM_AGABI	Q9p4t6 agaricus bi
36	535.5	46.4	205	1 SODM_CHLMU	Q9pka0 chlamydia m
37	529.5	45.9	206	1 SODM_CHLTR	O84296 chlamydia t
38	529	45.9	224	1 SODM_CHAFE	O96347 charybdis f
39	514.5	44.6	207	1 SODM_CHLPN	Q9z9c4 chlamydia p
40	511	44.3	203	1 SODM_BACAA	Q811w0 bacillus an
41	504.5	43.8	201	1 SODM_BACSU	P54375 bacillus su
42	503	43.6	203	1 SODM_XANCP	P53654 xanthomonas
43	496	43.0	203	1 SODM_BACCA	P28760 bacillus st
44	495	42.9	203	1 SODM_BACST	P00449 bacillus ca
45	492	42.7	202	1 SODM_LISMO	P28764 listeria mo

ALIGNMENTS

RESULT 1
SODM_GANMI
ID SODM_GANMI STANDARD; PRT; 200 AA.
AC Q92429; 1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
OS Ganoderma microsporium
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Ganodermataceae; Ganoderma.
OX NCBI_TaxID=34462;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RSB 0821;
RA Wang H.F.;
RL Thesis (1996), National Taiwan University, Taiwan.
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.

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or send an email to license@isb-sib.ch).

EMBL; U56403; AAB07360.1; -;
EMBL; U56127; AAB16782.1; -;
HSSP; P04179; IABW.
InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe_1.
DR Pfam; PF02777; sodfe_C_1.
DR PRINTS; PR01703; MNSODISWTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
DR Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 200 SUPEROXIDE DISMUTASE [MN].
FT METAL 27 27 MANGANESE (BY SIMILARITY).
FT METAL 72 72 MANGANESE (BY SIMILARITY).
FT METAL 161 161 MANGANESE (BY SIMILARITY).
FT METAL 165 165 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 200 AA; 22170 MW; E39DFCTE1708961F CRC64;

Query Match 64.9%; Score 748.5; DB 1; Length 200;
Best Local Similarity 71.6%; Pred. No. 1.2e-59;
Matches 141; Conservative 24; Mismatches 23; Indels 9; Gaps 3;

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QY 27 HTLPPEYDALPSPISKEIMTLHTKHTQYVNGLNABESYS-AAVGKEDVLTQVKL 85
DB 3 HVLEPDLPAYNLPSPISQOIMELHKKHTQYVNSLNABEQAKASTPKS-----RIAL 58
QY 86 QSALKFNGGGHINSLFWKNIAPYGE-----EATLSEGLPKALBESFGSPFAFKKXFN 141
DB 59 QSALKFNGGGHINSLFWKNIAPAKSEKGGKNGALADGPKLSALEQNGWSVDNFIKEFNA 118
QY 142 DTAAVQSGWGLNGINLPKLEVTITANOPDLTHPIIGVDIWEHAFYLOYKXKVPDY 201
DB 119 TTAATQSGWGLNGINLPATKLEITTTANOPDLTHPIIGVDIWEHAFYLOYKXKVPDY 178
QY 202 LAAVKSVINYKEAERL 218
DB 179 LAATWIVINFEAERL 195

RESULT 2
SODM MOUSE STANDARD; PRT; 222 AA.
AC P09671; Q64670; Q8VEM5;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-JUL-1998 (Rel. 36, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2 OR SOD-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=87091590; PubMed=3797253;
RA Hallowell R.A., Mullenbach G.T., Stempien M.M., Bell G.I.;
RT "Sequence of a cDNA coding for mouse manganese superoxide dismutase.";
RL Nucleic Acids Res. 14:9539-9539(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c, and C3H;
RX MEDLINE=94010326; PubMed=8406027;
RA Sun Y., Heganyer G., Colburn N.M.;
RT "Sequence of manganese superoxide dismutase-encoding cDNAs from
multiple mouse organs.";
RL Gene 131:301-302(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95180711; PubMed=7875582;
RA Jones P.L., Kucera G., Gordon H.M., Boss J.M.;
RT "Cloning and characterization of the murine manganese superoxide
dismutase-encoding gene.";
RL Gene 153:155-161(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95337589; PubMed=7613035;
RA Disilvestre D., Kleberger S.R., Johns J., Levitt R.C.;
RT "Structure and DNA sequence of the mouse MnSOD gene.";
RL Mamm. Genome 6:281-284(1995).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriin L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.F.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
family.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X04972; CAA28645.1; -
DR EMBL; Z18857; CAA79308.1; -
DR EMBL; L35528; AAB60902.1; -
DR EMBL; L35526; AAB60902.1; JOINED.
DR EMBL; L35527; AAB60902.1; JOINED.
DR EMBL; S78846; AAB34899.1; -
DR EMBL; S78832; AAB34899.1; JOINED.
DR EMBL; S78842; AAB34899.1; JOINED.
DR EMBL; S78844; AAB34899.1; JOINED.
DR EMBL; AK002428; BAB22095.1; -
DR EMBL; AK002534; BAB22170.1; -
DR EMBL; AK012354; BAB28183.1; -
DR EMBL; BC010548; AAH10548.1; -
DR EMBL; BC018173; AAH18173.1; -
DR FIR; I57023; I57023.
DR HSSP; P04179; IABM.
DR SWISS-2DPAGE; P09671; MOUSE.
DR MGD; MGI:983352; Sod2.
DR GO; GO:0008383; P:manganese superoxide dismutase activity; IMP.
DR GO; GO:0006801; P:superoxide metabolism; IMP.
DR InterPro; IPR001189; SOD1dmutase.
DR Pfam; PF00081; sodfe; 1.

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DR Pfam; PF02777; sodfe C; 1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR PRODOM; PD000475; SODISMUTASE; 1.
 DR PROSITE; PS00088; SOD MN; 1.
 KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
 KW Transit peptide.
 FT TRANSIT 1 24 MITOCHONDRION.
 FT CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
 FT METAL 50 50 MANGANESE (BY SIMILARITY).
 FT METAL 98 98 MANGANESE (BY SIMILARITY).
 FT METAL 183 183 MANGANESE (BY SIMILARITY).
 FT METAL 187 187 MANGANESE (BY SIMILARITY).
 FT CONFLICT 5 5 A -> G (IN REF. 5; AAH18173).
 FT CONFLICT 18 18 G -> V (IN REF. 1).
 FT CONFLICT 138 138 V -> M (IN REF. 1 AND 3).
 SQ SEQUENCE 222 AA; 24603 MW; 9AE804C55A8357D9 CRC64;
 Query Match 55.0%; Score 634.5; DB 1; Length 222;
 Best Local Similarity 55.6%; Pred. No. 2e-49;
 Matches 124; Conservative 30; Mismatches 62; Indels 7; Gaps 3;
 QY 1 MSVRASLSVSRQTFVAPAAQFIRAKHTLPDPYVADALEPSISKETMLHHTKHQTVV 60
 Db 1 MLCRAACSTGRKLPVAGAGS-RHKHSUPDLPDYGALEPHINAQIMQLHSHKHAAYV 59
 QY 61 NGLNAAEESYSAAVGKEDVLTQVKLSALKFNGGGHINHSFLWKNLAPYGESEATLSEGP 120
 Db 60 NNLNATEEKYHEALAKGDVTTQVALQPAKFNGGGHINHTFNTNLSPKGGGE---PKGE 116
 QY 121 LKKAIESFGSFEAFKKFNADTAAVQSGSGWGLGNPLTKLEVTTTANQDPL---LTH 177
 Db 117 LLEAIKRDGFSFEKFEKLTAVSVGVQSGSGWGLGNKEQGRQIAACSNQDPLQGTG 176
 QY 178 IPTIGVDIWEHAFYLOKVKPDYLAAVSVINYNKEAEARLQA 220
 Db 177 IFLLGIDVWEHAYLYQKVRPDYLAIVNINWNVNTERYTA 219
 RESULT 3
 SODM RAT STANDARD; PRT; 222 AA.
 ID SODM RAT STANDARD; PRT; 222 AA.
 AC P07895;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 GN SOD2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=88096516; PubMed=3697077;
 RA Ho Y.-S., Crapo J.D.;
 RT "Nucleotide sequences of cDNAs coding for rat manganese-containing superoxide dismutase."
 RL Nucleic Acids Res. 15:10070-10070(1987).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=91159005; PubMed=2001291;
 RA Ho Y.-S., Howard A.J., Crapo J.D.;
 RT "Molecular structure of a functional rat gene for manganese-containing superoxide dismutase."
 RL Am. J. Respir. Cell Mol. Biol. 4:278-286(1991).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
 CC -!- SUBUNIT: Homotrimer.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.

CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.
 CC -----
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 CC -----
 CC EMBL; Y00497; CAA68549.1; --
 DR EMBL; X56600; CAA39937.1; --
 DR PIR; S21661; DSRTN.
 DR HSSP; P04179; IAEH.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe C; 1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR PRODOM; PD000475; SODISMUTASE; 1.
 DR PROSITE; PS00088; SOD MN; 1.
 KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
 KW Transit peptide.
 FT TRANSIT 1 24 MITOCHONDRION.
 FT CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
 FT METAL 50 50 MANGANESE (BY SIMILARITY).
 FT METAL 98 98 MANGANESE (BY SIMILARITY).
 FT METAL 183 183 MANGANESE (BY SIMILARITY).
 FT METAL 187 187 MANGANESE (BY SIMILARITY).
 FT CONFLICT 167 167 Q -> H (IN REF. 1).
 SQ SEQUENCE 222 AA; 24674 MW; 8CCC1E0E857B3138 CRC64;
 Query Match 55.0%; Score 634.5; DB 1; Length 222;
 Best Local Similarity 55.4%; Pred. No. 2e-49;
 Matches 123; Conservative 30; Mismatches 58; Indels 11; Gaps 4;
 QY 1 MSVRASLSVSRQTFVAPAAQFI--RAKHTLPDPYVADALEPSISKETMLHHTKHQ 58
 Db 1 MLCRAACSAARR--LGPAASTAGSRHKHSLDLPDYGALEPHINAQIMQLHSHKHAT 57
 QY 59 YVNGLNAAEESYSAAVGKEDVLTQVKLSALKFNGGGHINHSFLWKNLAPYGESEATLSE 118
 Db 58 YVNNLVNTEEKYHEALAKGDVTTQVALQPAKFNGGGHINHSIFWNTNLSPKGGGE---PK 114
 QY 119 GPLKKAIESFGSFEAFKKFNADTAAVQSGSGWGLGNPLTKLEVTTTANQDPL---L 175
 Db 115 GELLEAIKRDGFSFEKFEKLTAVSVGVQSGSGWGLGNKEQGRQIAACSNQDPLQGT 174
 QY 176 THIPIIGVDIWEHAFYLOKVKPDYLAAVSVINYNKEAEAR 217
 Db 175 GLIPLIGIDVWEHAYLYQKVRPDYLAIVNINWNVNVSQR 216
 RESULT 4
 SODM BOVIN STANDARD; PRT; 222 AA.
 ID SODM BOVIN STANDARD; PRT; 222 AA.
 AC P41376;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
 GN SOD2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)_TaxID=9913;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94121934; PubMed=8292376;
 RA Meyrick B., Magnuson M.A.;
 RT "Identification and functional characterization of the bovine

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RT  manganous superoxide dismutase promoter.";
RL  Am. J. Respir. Cell Mol. Biol. 10:113-121(1994).
CC  -!- FUNCTION: Destroys radicals which are normally produced within the
CC  cells and which are toxic to biological systems.
CC  -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC  -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC  -!- SUBUNIT: Homotetramer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC  -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC  family.
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EMBL; L22092; AAA30655.1; ALT_INIT.
EMBL; L22093; AAA30656.1; -.
EMBL; S67818; AAC60522.2; -.
EMBL; S67819; AAD14001.1; -.
PIR; I51918; I51918.
HSSP; P04179; IABM.
InterPro: IPR001189; SODismutase.
Pfam; PF00081; sodfe_1.
Pfam; PF02777; sodfe_C_1.
PRINTS; PR01703; MNSODISMTASE.
ProDom; PD000475; SODismutase; 1.
PROSITE; PS00088; SOD MN; 1.
Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
Transit peptide.
KW TRANSIT
FT CHAIN 1 24 MITOCHONDRION (BY SIMILARITY).
FT METAL 25 222 SUPEROXIDE DISMUTASE [MN].
FT METAL 50 50 MANGANESE (BY SIMILARITY).
FT METAL 98 98 MANGANESE (BY SIMILARITY).
FT METAL 183 183 MANGANESE (BY SIMILARITY).
FT METAL 187 187 MANGANESE (BY SIMILARITY).
FT CONFLICT 8 8 S -> R (IN REF. 1; AAD14001).
FT CONFLICT 90 90 F -> V (IN REF. 1; AAC60522).
SQ SEQUENCE 222 AA; 24638 MW; 806CC3FCB1A74413 CRC64;
Query Match 54.6%; Score 629.5; DB 1; Length 222;
Best Local Similarity 54.3%; Pred. No. 5.5e-49;
Matches 121; Conservative 32; Mismatches 63; Indels 7; Gaps 3;
QY 1 MSVRASLSVSRTQTFVAPAAFOIRAKHTLPPELAYDALEPSISKEIMTLHTKHQTYV 60
Db 1 MLSRAACST-SRRLLVPALSVLSGRQKHSPLPDLPYDYGALPHINAQIMQLHSHKHAAYV 59
QY 61 NGLNAAESYSNAVGKEDVLTQVKLSALKFNGGCHINHSLFWKNIAPYGSBEATLSEGP 120
Db 60 NNLNVAEEKYREALEKGDVTAQIALQPALKFNKGCHINHSLFWKNIAPYGSBEATLSEGP 116
QY 121 LKKAITEESFGSFEAPKPKFNADTAQVSGGCMGLNPLTKLEVTTTANQDPL---LTH 177
Db 117 LLEAIRDFGSPAKFEKLTATVSGVGSGGCMGLNFKNKGQGLQIAACSNQDPLQGTGTL 176
QY 178 IPIIGDIWEHAFYLYQKNVKPDYLLAAVMSVINYKEAEARLQA 220
Db 177 IPLLIGDIWEHAFYLYQKNVKPDYLLKAIWVNIWENVATRYTA 219
RESULT 5
SODM HUMAN STANDARD; PRT; 222 AA.
AC P04179; P78434; Q16792; Q9P223;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBT_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89076921; PubMed=2462451;
RA Wispe J.R., Clark J.C., Burhans M.S., Kropp K.E., Korfhagen T.R.,
RA Whitsett J.A.;
RT "Synthesis and processing of the precursor for human
RT manganese superoxide dismutase.";
RL Biochim. Biophys. Acta 994:30-36(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88067716; PubMed=3684581;
RA Beck Y., Oren R., Amit B., Levanon A., Gorecki M., Hartman J.R.;
RT "Human Mn superoxide dismutase cDNA sequence.";
RL Nucleic Acids Res. 15:9076-9076(1987).
RN [3]
RP SEQUENCE FROM N.A.; AND VARIANT VAL-16.
RX MEDLINE=88289364; PubMed=3399391;
RA Heckl K.;
RT "Isolation of cDNAs encoding human manganese superoxide dismutase.";
RL Nucleic Acids Res. 16:6224-6224(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=88152250; PubMed=2831093;
RA Ho Y.-S., Crapo J.D.;
RT "Isolation and characterization of complementary DNAs encoding human
RT manganese-containing superoxide dismutase.";
RL FEBS Lett. 229:256-260(1988).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Colon;
RX MEDLINE=91105727; PubMed=1988135;
RA St Clair D.K., Holland J.C.;
RT "Complementary DNA encoding human colon cancer manganese superoxide
RT dismutase and the expression of its gene in human cells.";
RL Cancer Res. 51:939-943(1991).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=91027939; PubMed=1699607;
RA Church S.L.;
RT "Manganese superoxide dismutase: nucleotide and deduced amino acid
RT sequence of a cDNA encoding a new human transcript.";
RL Biochim. Biophys. Acta 1087:250-252(1990).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=95217333; PubMed=7702755;
RA Wan X.S., Devalaraja M.N., St Clair D.K.;
RT "Molecular structure and organization of the human manganese
RT superoxide dismutase gene.";
RL DNA Cell Biol. 13:1127-1136(1994).
RN [8]
RP SEQUENCE OF 25-222.
RX MEDLINE=85030346; PubMed=6386798;
RA Barra D., Schinina M.E., Simmaco M., Bannister J.V., Bannister W.H.,
RA Rotilio G., Bossa F.;
RT "The primary structure of human liver manganese superoxide
RT dismutase.";
RL J. Biol. Chem. 259:12595-12601(1984).
RN [9]
RP SEQUENCE OF 25-39.
RX TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
RN [10]
RP SEQUENCE OF 25-39.
RX TISSUE=Heart;

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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1)
(Mn-SOD).
GN SOD2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA MEDLINE=9261591; PubMed=10331206;
RX Ishida N., Katayama Y., Sato F., Hasegawa T., Mukoyama H.;
RT "The cDNA sequences of equine antioxidative enzyme genes Cu/Zn-SOD and
Mn-SOD, and these expressions in equine tissues.";
RL J. Vet. Med. Sci. 61:291-294(1999).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
family.
CC
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CC
CC EMBL; AB001693; BAA76922.1; -.
DR HSP; P04179; IABM.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sofde; 1.
DR Pfam; PF02777; sofde C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR PRODOM; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
KW Transit peptide.
FT TRANSIT 1 24 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 25 222 SUPEROXIDE DISMUTASE [MN].
FT METAL 50 50 MANGANESE (BY SIMILARITY).
FT METAL 98 98 MANGANESE (BY SIMILARITY).
FT METAL 183 183 MANGANESE (BY SIMILARITY).
FT METAL 187 187 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 222 AA; 24739 MW; 93A069481944E98C CRC64;
Query Match 53.4%; Score 615.5; DB 1; Length 222;
Best Local Similarity 52.9%; Pred. No. 9.8e-48;
Matches 118; Conservative 32; Mismatches 66; Indels 7; Gaps 3;
QY 1 MSVRASLSVSRQTFVAPAAQIRAKHTLPELPYADALEPSISKELMTLHHTKHQTVV 60
DB 1 MLCRAACST-SRKLVPALGSGSRQKSLPDLQYDYGALPEYINAIQMLHSHKHAAYV 59
QY 61 NGLNAABESYAAVKGEDVLTQVKLQSKALFKNGGGHINHSFLFWKNLAPYSGEATLSBGP 120
DB 60 NNLNVTEKYQALAKGVDVTAQIALQALPKFKNGGGHINHTFTWNLSPNGGGE---PKGK 116
QY 121 LKKAATESFGSPFAKFKFNADTAQVQSGWGLGNPLTKLEVTITANQDPL---LTH 177
DB 117 LLDALIKRDFGDFKFKELTAVSAGVQSGWGLGNQDKQGLQVACPNQDPLQGTGL 176
QY 178 IPIIGVDIWEHAFYLOYNKVPDYLAAVMSVINYKEAEARLQA 220
DB 177 IPIIGVDIWEHAFYLOYNKVPDYLAAVMSVINYKEAEARLQA 219

RESULT 7
SODM_MACFA
ID SODM_MACFA STANDARD; PRT; 198 AA.
AC Q8HXP3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
GN SOD2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
superoxide dismutases.";
RL Gene 296:99-109(2002).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
family.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; AB087278; BAC20357.1; ALT_INIT.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sofde; 1.
DR Pfam; PF02777; sofde C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR PRODOM; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT METAL 26 26 MANGANESE (BY SIMILARITY).
FT METAL 74 74 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 198 AA; 22209 MW; FB4F6B063190E5CC CRC64;
Query Match 53.3%; Score 615; DB 1; Length 198;
Best Local Similarity 56.6%; Pred. No. 9.4e-48;
Matches 112; Conservative 27; Mismatches 53; Indels 6; Gaps 2;
QY 26 KHTLPYADALEPSISKELMTLHHTKHQTVVNGLNAAEESYAAVKGEDVLTQVKL 85
DB 1 KHSLEPDLPYDYGALPEYINAIQMLHSHKHAAYNNLVTEKYQALAKGVDVTAQIAL 60
QY 86 QSKALFKNGGGHINHSFLFWKNLAPYSGEATLSBGLPKKAIESFGSPFAKFKFNADTAA 145
DB 61 QPALKFKNGGGHINHSIFWNLSPNGGGE---PKGELLEAIKRDGFSFKFKELTAASVG 117
QY 146 VQSGWGLGNPLTKLEVTITANQDPL---LTHPIIGVDIWEHAFYLOYNKVPDYLA 202
DB 118 VQSGWGLGNKKGKQGLQIAACPNQDPLQGTGLIPIIGVDIWEHAFYLOYNKVPDYLA 177
QY 203 AAVMSVINYKEAEARLQA 220
DB 178 KAIWNVINWENVERIYA 195

```

RESULT 8
SODM_MACFU
ID _SODM_MACFU STANDARD; PRT; 198 AA.
AC Q8HXP4;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
GN SOD2.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RT superoxide dismutases.";
RL Gene 296:99-109(2002).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB087277; BAC20356.1; ALT_INIT.
CC InterPro; IPR001189; SODismutase.
CC Pfam; PF00081; sodfe; 1.
CC PRINTS; PR01703; MNSODISMASE.
CC ProDom; PD000475; SODismutase; 1.
CC PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT METAL 26 26 MANGANESE (BY SIMILARITY).
FT METAL 74 74 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 198 AA; 22209 MW; FB4F6B063198E5CC CRC64;

Query Match 53.3%; Score 615; DB 1; Length 198;
Best Local Similarity 56.6%; Pred. No. 9.4e-48;
Matches 112; Conservative 27; Mismatches 53; Indels 6; Gaps 2;

QY 26 KHTLPPLVAYDALEPSISKEIMTLHTKHQTYNGLNAAEESYSAAYGKEDVLTQVKL 85
DB 1 KHSPLDLPDYDGALEPHINAQIMQLHSHKHAAYVNNLVNTEKYQEALAKGDVTAQIAL 60

QY 86 QSALKFNGGGCHNHSIFWKNLAPYGSSEATLSGPKLKAIESFGSFEAFKKFNADTAA 145
DB 61 QPALKFNGGGCHNHSIFWNLSPNGGGE---PKGELLEAIKRDGSGFEKFKLTAAVSG 117

QY 146 VQSGGWMGLNPLTKKLEVTITANQDPL---LTHPIIGVDIWEHAFYLYQKNVXPDYL 202
DB 118 VQSGGWMGLGFNKGKRGQLQIAACPNQDPLQGTGTLPLIGIDVWEHAFYLYQKNVXPDYL 177

QY 203 AAVWSVINYKEAEARLQA 220
DB 178 KAIWNVINWENVTERYMA 195

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RESULT 9
SODM_MACMU
ID _SODM_MACMU STANDARD; PRT; 198 AA.
AC Q8HXP2;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
GN SOD2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
RT superoxide dismutases.";
RL Gene 296:99-109(2002).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB087279; BAC20358.1; ALT_INIT.
CC InterPro; IPR001189; SODismutase.
CC Pfam; PF00081; sodfe; 1.
CC PRINTS; PR01703; MNSODISMASE.
CC ProDom; PD000475; SODismutase; 1.
CC PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT METAL 26 26 MANGANESE (BY SIMILARITY).
FT METAL 74 74 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 198 AA; 22209 MW; FB4F6B063198E5CC CRC64;

Query Match 53.3%; Score 615; DB 1; Length 198;
Best Local Similarity 56.6%; Pred. No. 9.4e-48;
Matches 112; Conservative 27; Mismatches 53; Indels 6; Gaps 2;

QY 26 KHTLPPLVAYDALEPSISKEIMTLHTKHQTYNGLNAAEESYSAAYGKEDVLTQVKL 85
DB 1 KHSPLDLPDYDGALEPHINAQIMQLHSHKHAAYVNNLVNTEKYQEALAKGDVTAQIAL 60

QY 86 QSALKFNGGGCHNHSIFWKNLAPYGSSEATLSGPKLKAIESFGSFEAFKKFNADTAA 145
DB 61 QPALKFNGGGCHNHSIFWNLSPNGGGE---PKGELLEAIKRDGSGFEKFKLTAAVSG 117

QY 146 VQSGGWMGLNPLTKKLEVTITANQDPL---LTHPIIGVDIWEHAFYLYQKNVXPDYL 202
DB 118 VQSGGWMGLGFNKGKRGQLQIAACPNQDPLQGTGTLPLIGIDVWEHAFYLYQKNVXPDYL 177

QY 203 AAVWSVINYKEAEARLQA 220
DB 178 KAIWNVINWENVTERYMA 195

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RESULT 10

SODM_HYLLA STANDARD; PRT; 198 AA.
 ID SODM_HYLLA STANDARD; PRT; 198 AA.
 AC Q8HXP5;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
 GN SOD2.
 OS Hylobates lar (Common gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=9580;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22271545; PubMed=12383507;
 RA Fukuhara R., Tezuka T., Kageyama T.;
 RT "Structure, molecular evolution, and gene expression of primate
 RT superoxide dismutases.";
 RL Gene 296:99-109(2002).

CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
 CC -!- SUBUNIT: Homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
 CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 CC family.

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DR EMBL; AB087276; BAC20355.1; ALT INIT.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe; C; 1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD MN; 1.
 KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
 FT METAL 26 26 MANGANESE (BY SIMILARITY).
 FT METAL 74 74 MANGANESE (BY SIMILARITY).
 FT METAL 159 159 MANGANESE (BY SIMILARITY).
 FT METAL 163 163 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 198 AA; 22234 MW; E266AFBBDB34566 CRC64;

Query Match 53.0%; Score 611; DB 1; Length 198;

Best Local Similarity 56.1%; Pred. No. 2.1e-47;

Matches 111; Conservative 27; Mismatches 54; Indels 6; Gaps 2;

QY 26 KHTLPPELAYDALEPSISKEITMLHTKHQTYVNGLNAAEESYSAAGKEDVLTQVKL 85
 DB 1 KHSFLDPLDYGALEPHINAQIMQLHSHKHAAYVNNLVNTEEKYQALAKGDVTAQAL 60
 QY 86 QSAKFNGGGGHINSLFWKNLAPYSGEATISEGLPKAIEESFGSFEAFKKFNADTAA 145
 DB 61 QPALKFNGGGGHINSLFWKNLAPYSGEATISEGLPKAIEESFGSFEAFKKFNADTAA 117
 QY 146 VQSGGWMGLGNPLTKLEVTNTANQDPL---LTHPIIGVDIWEHAFYLYQKNRPDYL 202
 DB 118 VQSGGWMGLGNPLTKLEVTNTANQDPL---LTHPIIGVDIWEHAFYLYQKNRPDYL 177
 QY 203 AAVWSVINYKEAEARLQA 220
 DB 178 KAIWNVINWENTERYMA 195

RESULT 11

SODM_PANTR STANDARD; PRT; 198 AA.
 ID SODM_PANTR STANDARD; PRT; 198 AA.
 AC Q8HX7;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
 GN SOD2.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22271545; PubMed=12383507;
 RA Fukuhara R., Tezuka T., Kageyama T.;
 RT "Structure, molecular evolution, and gene expression of primate
 RT superoxide dismutases.";
 RL Gene 296:99-109(2002).

CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
 CC -!- SUBUNIT: Homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
 CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 CC family.

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DR EMBL; AB087274; BAC20353.1; ALT INIT.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR Pfam; PF02777; sodfe; C; 1.
 DR PRINTS; PR01703; MNSODISMUTASE.
 DR ProDom; PD000475; SODismutase; 1.
 DR PROSITE; PS00088; SOD MN; 1.

KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
 FT METAL 26 26 MANGANESE (BY SIMILARITY).
 FT METAL 74 74 MANGANESE (BY SIMILARITY).
 FT METAL 159 159 MANGANESE (BY SIMILARITY).
 FT METAL 163 163 MANGANESE (BY SIMILARITY).
 SQ SEQUENCE 198 AA; 22204 MW; F772EABBA6A9F4CD CRC64;

Query Match 52.9%; Score 610; DB 1; Length 198;

Best Local Similarity 56.1%; Pred. No. 2.6e-47;

Matches 111; Conservative 27; Mismatches 54; Indels 6; Gaps 2;

QY 26 KHTLPPELAYDALEPSISKEITMLHTKHQTYVNGLNAAEESYSAAGKEDVLTQVKL 85
 DB 1 KHSFLDPLDYGALEPHINAQIMQLHSHKHAAYVNNLVNTEEKYQALAKGDVTAQAL 60
 QY 86 QSAKFNGGGGHINSLFWKNLAPYSGEATISEGLPKAIEESFGSFEAFKKFNADTAA 145
 DB 61 QPALKFNGGGGHINSLFWKNLAPYSGEATISEGLPKAIEESFGSFEAFKKFNADTAA 117
 QY 146 VQSGGWMGLGNPLTKLEVTNTANQDPL---LTHPIIGVDIWEHAFYLYQKNRPDYL 202
 DB 118 VQSGGWMGLGNPLTKLEVTNTANQDPL---LTHPIIGVDIWEHAFYLYQKNRPDYL 177
 QY 203 AAVWSVINYKEAEARLQA 220
 DB 178 KAIWNVINWENTERYMA 195

RESULT 12

```
SODM_PONPY STANDARD; PRT; 198 AA.
ID AC Q8HXP6;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SOD2.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22271545; PubMed=12383507;
RA Fukuhara R., Tezuka T., Kageyama T.;
RT "Structure, molecular evolution, and gene expression of primate
superoxide dismutases.";
RL Gene 296:99-109(2002).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
family.
CC -----
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CC -----
CC EMBL: AB087275; BAC20354.1; ALT INIT.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodfe_C_1.
DR Pfam: PF02777; sodfe_C_1.
DR PRINTS: PR01703; MNSODISMUTASE.
DR ProDom: PD000475; SODismutase; 1.
DR PROSITE: PS00088; SOD MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
FT METAL 26 26 MANGANESE (BY SIMILARITY).
FT METAL 74 74 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 198 AA; 22204 MW; F772EABBA6A9F4CD CRC64;
Query Match 52.9%; Score 610; DB 1; Length 198;
Best Local Similarity 56.1%; Pred. No. 2.6e-47;
Matches 111; Conservative 27; Mismatches 54; Indels 6; Gaps 2;
QY 26 KHTLPPLPAYDALEPSISKEIMTLHTKHQTVNGLNAAESYSAAVGKEDVLTQVKL 85
DB 1 KHSLEPDPYDYGALPRHINAIQMLHSHKHAAYVNNLVNTEKYQALAKGVDVTAQIAL 60
QY 86 QSALKFNGGGHINSLFWKLNAPYSGSEATLSBGLPKKAIEESFGSPFAFKKFNADTAA 145
DB 61 QPALKFNGGGHINHSIPWNLSPNGGGE---PKGELLEAIKROFGSPDKFKELTAASVG 117
QY 146 VQSGGWGLGNPLTKKLEVTITANQDPL---LTHPIIGVDVWEHAFYLOYKKNRPDYL 202
DB 118 VQSGGWGLGNFKRNGHGLQIAACPNDPQLOGTGTLPLGLGVDWEHAYLYQKKNRPDYL 177
QY 203 AAVWSVINYKEAEARLCA 220
DB 178 KAIWNVINWENVTERYNA 195
RESULT 13
SODM_ARATH
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SODM_ARATH STANDARD; PRT; 231 AA.
ID AC Q81235; Q9SRK3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).
GN SODA OR MSP1 OR AT3G10920 OR F9F8.26.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids;
OC eurosoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
MEDLINE=98440686; PubMed=9765550;
RA Kliebenstein D.J., Monde R.A., Last R.L.;
RT "Superoxide dismutase in Arabidopsis: an eclectic enzyme family with
disparate regulation and protein localization.";
RL Plant Physiol. 118:637-650(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
RA Partmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehert T.-H., Nordstiek G.,
RA Reichelt J., Schaefer M., Schoen O., Bargues M., Terol J., Clement J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauró C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.P.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Niernan W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asanizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.";
RL Nature 408:820-822(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Columbia;
MEDLINE=22954850; PubMed=14593172;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlín-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Arakawa T., Bann J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju N., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
genome.";
RL Science 302:842-846(2003).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
```

cells and which are toxic to biological systems.
 -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
 -!- SUBUNIT: Homotetramer (By similarity).
 -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.

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 EMBL; AF061518; AAC24832.1; -
 EMBL; AC009991; AAF01529.1; -
 EMBL; AY072495; AAL66910.1; -
 EMBL; AY059807; AAL24289.1; -
 PIR; T50827; T50827.
 HSRP; P04179; IABM.
 InterPro: IPR001189; SODismutase.
 Pfam; PF00081; sodfe, 1.
 Pfam; PF02777; sodfe C; 1.
 PRINTS; PR01703; MNSODISMUTASE.
 ProDom; PD000475; SODismutase; 1.
 PROSITE; PS00088; SOD MW; 1.
 Oxidoreductase; Metal-binding; Manganese; Mitochondrion;
 Transit peptide.
 TRANSIT 1 29 MITOCHONDRION (BY SIMILARITY).
 CHAIN 30 231 SUPEROXIDE DISMUTASE [MN].
 METAL 59 59 MANGANESE (BY SIMILARITY).
 METAL 103 103 MANGANESE (BY SIMILARITY).
 METAL 192 192 MANGANESE (BY SIMILARITY).
 METAL 196 196 MANGANESE (BY SIMILARITY).
 METAL 169 169 V -> F (IN REF. 1).
 CONFLICT 169 169
 SEQUENCE 231 AA; 25444 MW; 2DBD5560A9E8AD7D CRC64;

Query Match 52.6%; Score 606; DB 1; Length 231;
 Best Local Similarity 60.2%; Pred. No. 7.2e-47;
 Matches 115; Conservative 21; Mismatches 51; Indels 4; Gaps 1;

Qy 28 TLPELPAYDALEPSISKEIMTLHHTKHQTYVNGLNAAEESYSAAGKEDVLTQVKLQS 87
 Db 32 TLPLPDYDGALEPAISGEIMQIHQKHQYVTVNNALQQLQAVNKGDASTVVKLQS 91

Qy 88 ALKENGGGHINSLFWKNLAPYGSBEATLSEGLKKAIEESFGSFEAPKKFNADTAQV 147
 Db 92 AIKENGGGHVNHSIFWKNLAPSEGGGPPKGLSGLSAIDAHFGLGLVKMSAEGAAVQ 151

Qy 148 GSGWGLGNPLTKKLEVTITANODPLTH---IPIIGVDIWEHAFYLYQKNVKKPDYLA 203
 Db 152 GSGWVNLGLDKELKLVLDITANODPLTVTKGSLVPLVGLVDVWEHAFYLYQKNVRPEYLK 211

Qy 204 AVWSVINYKEA 214
 Db 212 NVWKVINWKYA 222

RESULT 14
 SODM_CALJA STANDARD; PRT; 198 AA.
 AC Q8HXPO;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
 GN SOD2.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
 OC Callithrix.

NCBI_TaxID=9483;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=22271545; PubMed=12383507;
 RX Fukuhara R., Tezuka T., Kageyama T.;
 RT "Structure, molecular evolution, and gene expression of primate
 superoxide dismutases.";
 RL Gene 296:99-109(2002).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 cells and which are toxic to biological systems.
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
 CC -!- SUBUNIT: Homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
 CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 family.

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 EMBL; AB087281; BAC20360.1; ALT INIT.
 InterPro; IPR001189; SODismutase.
 Pfam; PF00081; sodfe, 1.
 Pfam; PF02777; sodfe C; 1.
 PRINTS; PR01703; MNSODISMUTASE.
 ProDom; PD000475; SODismutase; 1.
 PROSITE; PS00088; SOD MW; 1.
 Oxidoreductase; Metal-binding; Manganese; Mitochondrion.
 METAL 26 26 MANGANESE (BY SIMILARITY).
 METAL 74 74 MANGANESE (BY SIMILARITY).
 METAL 159 159 MANGANESE (BY SIMILARITY).
 METAL 163 163 MANGANESE (BY SIMILARITY).
 SEQUENCE 198 AA; 22248 MW; E7F8960B8C56F2CA CRC64;

Query Match 52.5%; Score 605; DB 1; Length 198;
 Best Local Similarity 55.6%; Pred. No. 7.3e-47;
 Matches 110; Conservative 28; Mismatches 54; Indels 6; Gaps 2;

Qy 26 KHTPELPAYDALEPSISKEIMTLHHTKHQTYVNGLNAAEESYSAAGKEDVLTQVKL 85
 Db 1 KHSPLDLPYDGALEPHINQIMQLHSHKHAAVYNNLNDTEEKYKEALAKGDTAQLAL 60

Qy 86 QSALKFNGGGHINSLFWKNLAPYGSBEATLSEGLKKAIEESFGSFEAPKKFNADTAA 145
 Db 61 QPALKFNGGGHINHSIFWNLSPNGGGE---PKGELLEAIKRDGSGDFKFKERLTAASVG 117

Qy 146 VQSGWGLGNPLTKKLEVTITANODPL---LTHIPIIGVDIWEHAFYLYQKNVKKPDYL 202
 Db 118 VQSGWGLGNFNGKRGHGLQIAACPNQDPLQGTGTLIPLGLDGVWEHAFYLYQKNVRPDL 177

Qy 203 AAVWSVINYKEAEARLQA 220
 Db 178 KAIWNVINWENVTERYMA 195

RESULT 15
 SODM_CEBAP STANDARD; PRT; 198 AA.
 ID SODM_CEBAP
 AC Q8HXPL;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1).
 GN SOD2.
 OS Cebus apella (Brown-capped capuchin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
 OC NCBI_TaxID=9515;

```
RN SEQUENCE FROM N.A.
RP MEDLINE=22271545; PubMed=12383507;
RX Fukuhara R., Tezuka T., Kageyama T.;
RA "Structure, molecular evolution, and gene expression of primate
RT superoxide dismutases.";
RL Gene 296:99-109(2002).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB087280; BAC20359.1; ALT INIT.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe_1.
DR Pfam; PF02777; sodfe_C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Oxidoreductase; Metal-binding; Manganese; Mitochondrion..
FT METAL 26 26 MANGANESE (BY SIMILARITY).
FT METAL 74 74 MANGANESE (BY SIMILARITY).
FT METAL 159 159 MANGANESE (BY SIMILARITY).
FT METAL 163 163 MANGANESE (BY SIMILARITY).
SQ SEQUENCE 198 AA; 22248 MW; E7F8860B8C56F2CA CRC64;

Query Match 52.5%; Score 605; DB 1; Length 198;
Best Local Similarity 55.6%; Pred. No. 7.3e-47;
Matches 110; Conservative 28; Mismatches 54; Indels 6; Gaps 2;

QY 26 KHTLPPLPYDALEPSISKEIMTLHHTKHQTYVNGLNAAESYSAAVGKEDVLTQVKL 85
Db 1 KHSPLDLPYDYGALPHINAQIMQLHSHKHAAYVNNLNDTEKYKEALAKGDTVTAQIAL 60

QY 86 QSALKPFGGGHINHSLFWKNLAPYGESEATLSEGPLKKAIEBSFGSFEAPKKKFNADTAA 145
Db 61 QPALKFGGGHINHSLFTWNLSPNGGGE---PKGELLEAIKRDGSGDFKFKERLTAASVG 117

QY 146 VQSGGWGLGLNPLTKKLEVTITANODPL---LTHIPIIGVDIWEHAFYLYQKNVXPDYL 202
Db 118 VQSGGWGLGFGNKRGHGLQIAACPNODPLQGTTLGLIPLIGDIDWEHAYLYQKNVXPDYL 177

QY 203 AAVWSVINYKEAEARLQA 220
Db 178 KAINVINWENTERYWA 195
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Search completed: March 30, 2004, 17:14:38

Job time : 19 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2004, 17:09:18 ; Search time 26 Seconds
(without alignments)
821.328 Million cell updates/sec

Title: US-09-727-855b-5
Perfect score: 1153
Sequence: 1 MSVRASLSVSRSQTTFVAPAA.....AAVWSVINYKEARLQAAAL 222

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	634.5	55.0	222	1 DSRPN	superoxide dismuta
2	634.5	55.0	222	2 I57023	superoxide dismuta
3	629.5	54.6	222	1 I51918	superoxide dismuta
4	620	53.8	222	1 DSHUN	superoxide dismuta
5	614	53.3	231	2 T08181	superoxide dismuta
6	612.5	53.1	237	2 T50830	superoxide dismuta
7	601	52.1	231	2 T50827	superoxide dismuta
8	600	52.0	204	2 S65795	superoxide dismuta
9	600	52.0	228	2 T50828	superoxide dismuta
10	600	52.0	240	1 DSPMN	superoxide dismuta
11	596	51.7	233	2 T06258	superoxide dismuta
12	595	51.6	233	2 S39492	superoxide dismuta
13	592	51.3	228	2 S03639	superoxide dismuta
14	590.5	51.2	231	2 T04075	probable superoxid
15	590.5	51.2	231	2 T04075	probable superoxid
16	590.5	51.2	231	2 T04312	probable superoxid
17	590	51.2	233	2 B48684	superoxide dismuta
18	587	50.9	231	2 T06801	probable superoxid
19	584.5	50.7	221	2 JC5122	superoxide dismuta
20	584	50.7	235	2 S03839	superoxide dismuta
21	582	50.5	228	2 T08045	superoxide dismuta
22	581	50.4	205	2 T50829	superoxide dismuta
23	574	49.8	240	2 T47752	superoxide dismuta
24	574	49.8	241	2 T47752	superoxide dismuta
25	572	49.6	218	2 S52721	superoxide dismuta
26	570.5	49.5	232	2 C48684	superoxide dismuta
27	560	48.6	218	2 T50070	superoxide dismuta
28	558	48.4	233	2 A48684	superoxide dismuta
29	553	48.0	198	2 T09799	superoxide dismuta

30	548	47.5	187	2 T50832	superoxide dismuta
31	543.5	47.1	233	2 T09788	probable superoxid
32	535.5	46.4	207	2 A81688	superoxide dismuta
33	529.5	45.9	206	2 H71531	superoxide dismuta
34	514.5	44.6	207	2 B86498	superoxide dismuta
35	514.5	44.6	207	2 B72124	superoxide dismuta
36	504.5	43.8	226	2 B69709	superoxide dismuta
37	496	43.0	204	2 S22053	superoxide dismuta
38	495	42.9	204	1 DSBNSF	superoxide dismuta
39	492	42.7	202	2 JC1272	superoxide dismuta
40	492	42.7	202	2 AG1254	superoxide dismuta
41	491.5	42.6	196	2 A39223	superoxide dismuta
42	491.5	42.6	223	2 S48831	superoxide dismuta
43	491.5	42.6	223	2 S48832	superoxide dismuta
44	488	42.3	202	2 S20019	superoxide dismuta
45	488	42.3	202	2 AE1617	superoxide dismuta

ALIGNMENTS

RESULT 1

DSRN

superoxide dismutase (EC 1.15.1.1) (Mn) precursor - rat
C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 11-Jun-1999

C:Accession: S21661, S06310

R;Ho, Y.S.; Howard, A.J.; Crapo, J.D.

submitted to the EMBL Data Library, October 1990

A:Reference number: S21661

A:Accession: S21661

A:Molecule type: DNA

A:Residues: 1-222 <HOY1>

A:Cross-references: EMBL:X56600; NID:g57272; PIDN:CAA39937.1; PID:g57273

R;Ho, Y.S.; Crapo, J.D.

Nucleic Acids Res. 15, 10070, 1987

A:Title: Nucleotide sequences of cDNAs coding for rat manganese-containing superoxide dis

A:Reference number: S06310; MUID:88096516; PMID:3697077

A:Accession: S06310

A:Molecule type: mRNA

A:Residues: 1-166, 'H', 168-222 <HOY2>

A:Cross-references: EMBL:X00497; NID:g56690; PIDN:CAA68549.1; PID:g56691

A:Note: 167-Gln was also found

C:Genetics:

A:Gene: SOD2

A:Introns: 8/2; 76/1; 115/1; 175/1

C:Function:

A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C:Superfamily: superoxide dismutase (Mn)

C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase

F:1-24/Domain: transit peptide (mitochondrion) #status predicted <TNP>

F:25-222/Product: superoxide dismutase (Mn) #status predicted <MNT>

F:50,98,183,187/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 55.0%; Score 634.5; DB 1; Length 222;

Best Local Similarity 55.4%; Pred. No. 6.5e-49;

Matches 123; Conservative 30; Mismatches 58; Indels 11; Gaps 4;

QY 1 MSVRASLSVSRSQTTFVAPAFQI--RAKHTLPDLPVAYDALEPSISKEMTLHHTKHQT 58

Db 1 MLCRAACSGRR---LGPAASTAGSRHKSFLPDLPYDYGALPEHINAQIMQLHSHKHAT 57

QY 59 YVNGINAARESVSAAGKEDVLTQVKLSALPENGCGGHINHSIFWNLAAPYSGEATLSE 118

Db 58 YVNNLVNTEKHYHEALAKGDVTTQVALQPALPENGCGGHINHSIFWNLSFGKGE---PK 114

QY 119 GPLKKAIESFGSFEAFKKFNADTAAGVSGSGWGLGNPLTKKLEVTVTANODPL---L 175

Db 115 GELLEIAKDDFGSFEKFEKLTAVSVGVSGSGWGLGNFNKEQCRQIQIAACSNODPLQGT 174

QY 176 THPIIGVDIWEHAFYLYQYKNKVPDYLAADVSVINYKEABAR 217

Db 175 GLIPLIGIDWEHAYLYQYKNKVPDYLYKAIWNVINWENVSQR 216

```
151918
superoxide dismutase (EC 1.15.1.1) (Mn) precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 15-Oct-1996 #sequence_revision 15-Aug-1997 #text_change 21-Jul-2000
C:Accession: I51918; I64848; I64850
R:Meyrick, B.; Magnuson, M.A.
A:Title: Identification and functional characterization of the bovine manganous superoxide
dismutase
A:Reference number: 151918; MUID:94121934; PMID:8292376
A:Accession: I51918
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-222 <MEY1>
A:Cross-references: GB:L22092; NID:g498259; PIDN:AAA30655.1; PID:g498260
A:Accession: I64848
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <MEY2>
A:Cross-references: GB:L22093; NID:g498261; PIDN:AAA30656.1; PID:g552330
A:Accession: I64850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7, 'R' <MEY3>
A:Cross-references: GB:S67819; NID:g460572; PIDN:AAD14001.1; PID:g4261701
C:Genetics:
C:Gene: MnSOD
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:1-24/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:25-222/Product: superoxide dismutase (Mn) #status predicted <MAT>
F:50,98,183,187/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 54.6%; Score 629.5; DB 2; Length 222;
Best Local Similarity 54.3%; Pred. No. 1.8e-48;
Matches 121; Conservative 32; Mismatches 63; Indels 7; Gaps 3;

Qy 1 MSVRASLSVSROTFVAPAAQIRAKHTLPPEYDALPEPSISKEIMTLHHTKHQTYV 60
Db 1 MLSPAACT-SRRLVPALSVLGSQKSLPDLPDYDYGALPEPHINAQIMQLHSHKHAAYV 59

Qy 61 NGLNAEESYSAAVGKEDVLTQVKLSQALKPFGGHHNHSIFWNKLPYSGEATLSEGP 120
Db 60 NNLNAEEKYHEALAKGDVTTQVALQPALKFGGHHNHSIFWNLSFGGGE---PKGE 116

Qy 121 LKKAIESFGSFEAFKKFNADTAAGVSGSGWGLNPLTKLEVTITANODPL---LTH 177
Db 117 LLEAIKRDGFSFAKFEKLTAVSVGVSGSGWGLNPLTKLEVTITANODPL---LTH 176

Qy 178 IPIIGVDIWEHAFYLYQKNVDPYLAADVSVINYKEAEARLQA 220
Db 177 IPLLGDVWEHAYLYQKNVDPYLAADVSVINYKEAEARLQA 219

RESULT 4
DSHUN
superoxide dismutase (EC 1.15.1.1) (Mn) precursor [validated] - human
C:Species: Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 06-Feb-1995 #text_change 20-Apr-2000
C:Accession: S13162; S02272; S11756; S00356; S02230; S00663; A92447; I38033; A00520; A2777;
R:Church, S.L.
A:Title: Manganese superoxide dismutase: nucleotide and deduced amino acid sequence of a
human
A:Reference number: S13162; MUID:91027939; PMID:1699607
A:Accession: S13162
A:Molecule type: mRNA
A:Residues: 1-222 <CHU>
A:Note: cross-reference GB:M34665 cited in paper is not correct
R:Wise, J.R.; Clark, J.C.; Burhans, M.S.; Kropp, K.E.; Korfhagen, T.R.; Whitsett, J.A.
Biochim. Biophys. Acta 994, 30-36, 1989
A:Title: Synthesis and processing of the precursor for human manganous superoxide dismutase
A:Reference number: S02272; MUID:89076921; PMID:2462451
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```
157023
superoxide dismutase (EC 1.15.1.1) (Mn) precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Jun-1999
C:Accession: I57023; JC4047; S36129; A25581
R:DiSilvestre, D.; Kleeberger, S.R.; Johns, J.; Levitt, R.C.
Mamm. Genome 6, 281-284, 1995
A:Title: Structure and DNA sequence of the mouse MnSOD gene.
A:Reference number: I57023; MUID:95337589; PMID:7613035
A:Accession: I57023
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-222 <RES>
A:Cross-references: GB:S78846; NID:g1037119; PIDN:AAB34899.1; PID:g1037120
R:Jones, P.L.; Kucera, G.; Gordon, H.; Boss, J.M.
Gene 153, 155-161, 1995
A:Title: Cloning and characterization of the murine manganous superoxide dismutase-encod
ing cDNA
A:Reference number: JC4047; MUID:95180711; PMID:7875582
A:Accession: JC4047
A:Molecule type: DNA
A:Residues: 1-137, 'M', 139-222 <JON>
A:Cross-references: GB:I35525
R:Sun, Y.
submitted to the EMBL Data Library, November 1992
A:Reference number: S36129
A:Accession: S36129
A:Molecule type: mRNA
A:Residues: 1-222 <SUN>
A:Cross-references: EMBL:Z18857; NID:g288504; PIDN:CAA79308.1; PID:g288505
R:Hallewell, R.A.; Mullenbach, G.T.; Stempien, M.M.; Bell, G.I.
Nucleic Acids Res. 14, 9539, 1986
A:Title: Sequence of a cDNA coding for mouse manganese superoxide dismutase.
A:Reference number: A25581; MUID:87091590; PMID:3797253
A:Accession: A25581
A:Molecule type: mRNA
A:Residues: 1-17, 'V', 19-137, 'M', 139-222 <HAL>
A:Cross-references: GB:X04972; NID:g53449; PIDN:CAA28645.1; PID:g53450
C:Genetics:
C:Gene: Sod-2
C:Introns: 8/2; 76/1; 115/1; 175/1
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F:1-24/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:25-222/Product: superoxide dismutase (Mn) #status predicted <MAT>
F:50,98,183,187/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 55.0%; Score 634.5; DB 2; Length 222;
Best Local Similarity 55.6%; Pred. No. 6.5e-49;
Matches 124; Conservative 30; Mismatches 62; Indels 7; Gaps 3;

Qy 1 MSVRASLSVSROTFVAPAAQIRAKHTLPPEYDALPEPSISKEIMTLHHTKHQTYV 60
Db 1 MLCRAACSTGRRLGVPAGAAGS-RHKSLPDLPDYDYGALPEPHINAQIMQLHSHKHAAYV 59

Qy 61 NGLNAEESYSAAVGKEDVLTQVKLSQALKPFGGHHNHSIFWNKLPYSGEATLSEGP 120
Db 60 NNLNAEEKYHEALAKGDVTTQVALQPALKFGGHHNHSIFWNLSFGGGE---PKGE 116

Qy 121 LKKAIESFGSFEAFKKFNADTAAGVSGSGWGLNPLTKLEVTITANODPL---LTH 177
Db 117 LLEAIKRDGFSFAKFEKLTAVSVGVSGSGWGLNPLTKLEVTITANODPL---LTH 176

Qy 178 IPIIGVDIWEHAFYLYQKNVDPYLAADVSVINYKEAEARLQA 220
Db 177 IPLLGDVWEHAYLYQKNVDPYLAADVSVINYKEAEARLQA 219

RESULT 3
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C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; mitochondrion; oxidoreductases
F;1-24/Domain: transit peptide (mitochondrion) #status predicted <INP>
F;25-222/Product: superoxide dismutase (Mn) #status experimental <WAT>
F;50,98,183,187/Binding site: manganese (His, Asp, His) #status experimental

Query Match 53.8%; Score 620; DB 1; Length 222;
Best Local Similarity 53.6%; Pred. No. 1.3e-47;
Matches 118; Conservative 31; Mismatches 61; Indels 10; Gaps 4;

Qy 6 SLSSVSRTFVAPAAFOI--RAKHTLPELPYAYDALEPSISKEIMTLHHTKHQTYYNGL 63
Db :
5 AVCGTSRQ--LAPALGYLSGRQKHSPLDLPDYDGALPHINAQIMQLHSHKHAAYNNL 62
Qy 64 NABESYSAAVKGEVDLVTVKLQSALKFNKGCGGHINHSLFWKNLAPYGSBEATLSEGPLKK 123
Db :
63 NVTEKYQEALAKGDVTQAIALQPALKFNKGCGGHINHSIFWTNLSPNGGGE---PKGELLE 119
Qy 124 AIESPFGSFEAFKKFNADTAAVQSGGWLGUNPLTKKLEVTTTANODPL---LTHPI 180
Db :
120 AIKRDFGSDFKPEKLTAAASVGQSGWLGFGNKERGHLLQAACPNQDPLOGTGTLPL 179
Qy 181 IGVDIWEHAFYLQYNKVPDYLAAVMSVINYPEAEARLOA 220
Db :
180 LGIDWEHAYLYQYNKVPDYLKAINVINWENVIERYMA 219

RESULT 5
T08181
superoxide dismutase (EC 1.15.1.1) (Mn) - radish
C;Species: Raphanus sativus (radish)
C;Date: 16-Jul-1999 #sequence revision 16-Jul-1999 #text_change 20-Apr-2000
C;Accession: T08181
R;Kwon, S.I.; An, C.S.
submitted to the EMBL Data Library, April 1998
A;Reference number: Z16401
A;Accession: T08181
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-231 <KW>
A;Cross-references: EMBL:AF061133; NID:g3108344; PID:g3108345
C;Genetics:
A;Gene: sod
C;Function:
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F;55,103,192,196/Binding site: manganese (His, Asp, His) #status predicted

Query Match 53.3%; Score 614; DB 2; Length 231;
Best Local Similarity 57.5%; Pred. No. 4.6e-47;
Matches 122; Conservative 20; Mismatches 54; Indels 16; Gaps 2;

Qy 7 LSSVSRTFVAPAAFOIRAKHTLPELPYAYDALEPSISKEIMTLHHTKHQTYYNGLAA 66
Db :
23 LGSRSIQTF-----TLPDLPDYSALEPAISGEIMOIHQKHQAIVTYNNA 70
Qy 67 BESYSAAVKGEVDLVTVKLQSALKFNKGCGGHINHSLFWKNLAPYGSBEATLSEGPLKKAIE 126
Db :
71 LEQLDAQNVKGDASAVVKLQSAIKFNKGCGGHVNHSLFWKNLAPYKGGEGEPKGSGLGAID 130
Qy 127 ESFGSFEAFKKFNADTAAVQSGGWLGUNPLTKKLEVTTTANODPLLTH----IPILG 182
Db :
131 TSFGSLEGLVKNWSAEGAAGVQSGWWLGLDKELKLVVDTTTANQDPLVTKGGSLVPLVG 190
Qy 183 VDIWEHAFYLQYNKVPDYLAAVMSVINYPEA 214
Db :
191 IDVWEHAYLYQYNKVRPDYLNKVNWKVINYA 222

RESULT 6
T50830
superoxide dismutase (EC 1.15.1.1) (Mn) precursor, mitochondrial [similarity] - leafy sp

Dd 152 GSGWVGLDKLKKLVFDTTANQDPLVTKGGSLVPVLGVGDVWEHAYYLQYKNVRPBYLK 21

Qy 204 AVMSVINYPEA 214
 ||| |
Db 212 NWVKINWKYA 222

RESULT 8

S65795
superoxide dismutase [EC 1.15.1.1] (Mn) - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Mar-1999
C;Accession: S65795
R;Yuan, H.T.; Bingle, C.D.; Kelly, F.J.
Biochim. Biophys. Acta 1305, 163-171, 1996
A;Title: Differential patterns of antioxidant enzyme mRNA expression in guinea
A;Reference number: S65793; MUID:96180320; PMID:8597602
A;Accession: S65795
A;Molecule type: mRNA
A;Residues: 1-204 <YUA>
A;Cross-references: EMBL:U39843
C;Genetics:
A;Genome: nuclear
C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; mitochondrion; oxidoreductase
F;43,91,176,180/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 52.0%; Score 600; DB 2; Length 204;
Best Local Similarity 55.4%; Pred. No. 6.7e-46;
Matches 113; Conservative 27; Mismatches 58; Indels 6; Gaps 2;

Qy 9 SVSRQTFFAPAFQIRAKHTLPYPAYDALEPSISKEIWTLLHHTKHQTYVNGLNAAEE 68
Db 1 SASRLIAPALGILGRQRXHSUPDPDYGAQPCHINAIEIMQLHSHSKHAAYLANNLIAEE 60

Qy 69 SYSAAVKGEDVLTQKLQSALKFGGGGHINSFLWNKLNPYGSEATLSRGPLKKAETES 128
Db 61 KYQEALAGDVTAQAVALPALKFNGGGGHNSIFWTNLSPNGGE---PKGELLEAIKR D 177

Qy 129 FGSGFAFKKFNADTAACVGSGWGWLGNPTTKLEVTTTANQDPL---LTHPIPIIGVDI 185
Db 118 FGSDFKFEKLTAVSIVGVQGSGWGLGNKERGCLOIAAGSNQDPLQGTTLGPLLGIDV 177

Qy 186 WEHAFYLYQNKPDPDLAAVWSVI 209
Db 178 WEHAYYQLKNRPDYLRKWVI 201

RESULT 9

T50828
superoxide dismutase [EC 1.15.1.1] (Mn) 1 [similarity] - Prunus persica
C;Species: Prunus persica
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000
C;Accession: T50828
R;Bagnoli, F.

submitted to the EMBL Data Library, October 1999
A;Reference number: Z5247
A;Accession: T50828
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-228 <BAG>
A;Cross-references: EMBL:AJ238316; PIDN:CMB56851.1
C;Genetics:
A;Gene: sod
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F;52,100,189,193/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 52.0%; Score 600; DB 2; Length 228;
Best Local Similarity 55.9%; Pred. No. 7.8e-46;
Matches 119; Conservative 25; Mismatches 61; Indels 8; Gaps 3;

Query Match	51.7%;	Score	596;	DB	2;	Length	231;
Best Local Similarity	55.2%;	Pred.	No. 1.8e-45;				
Matches	116;	Conservative	23;	Mismatches	65;	Indels	6;
						Caps	2;

A;Molecule type: mRNA
A;Residues: 1-240 <WON>
A;Cross-references: EMBL:X60170; NID:q20901; PIDN:CAA42737.1; PID:q20902

Query Match	52.0%	Score 600;	DB 1;	Length 240;
Best Local Similarity	54.3%	Pred. No. 8.4e-46;		
Matches 125;	Conservative	28;	Mismatches 51;	Indels 26;
Gaps 6;				

A;Residues: 1-233 <MLA>
 A;Cross-references: GB:L11707; NID:G348136; PIDN:AAA16792.1; PID:G348137
 C;Function:

C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F:58,103,192,196/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match	51.6%;	Score 595;	DB 2;	Length 233;
Best Local Similarity	53.3%;	Pred. NO. 2.2e-45;		
Matches 121;	Conservative	30;	Mismatches 58;	Indels 18;
Gaps 5;				

[illegible]

56 H Q K H Q Y I T I N Y K A L S Q L N D A I E K G D S A A V V L Q S A I K F N G G G V H N S I F W K N L A P V R E 115

Db

112 E A T L S G P L K A I E E S F G S F E A F K K F N A D T A A V Q S G H G W L C I N P L T Y K K L E V T T A N Q 171

QY

116 G G G E L P H G S L G W A I D A D F G S L E K L I Q L M N E G A R L Q S G W V I A L D K E L K K I V V E T T A N Q 175

Db

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QY      172  DPLLTH-----IPITGVDIWEHAFYLYQYKNVKPQVLAAYWVSVINKEA  214
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
      176  DPLVTKGPTLVPLLGIDVWEHAFYLYQYKNVVRPDKNIWKVMNWKYA  222

Db

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RESULT 13

Search completed: March 30, 2004, 17:10:58
Job time : 27 secs